

GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: September 4, 2002, 16:09:21 : Search time 71.77 Seconds

Perfect score: US-09-052-089A-1  
Sequence: 1 MPIRACLTCSDFFDHSRDV..... VRVKTVPSPSLFOAKUDTFLWS 469

Title: US-09-052-089A-1

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs., 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : Swissprot\_40;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	192.5	8.1	1938	1 MYHD_HUMAN	09uhx3 homo sapien
2	187.5	7.9	2663	1 CENE_HUMAN	Q02224 homo sapien
3	183.5	7.7	1957	1 YD86_SCHPO	Q10411 schizosacch
4	182.5	7.7	1290	1 VDP_HUMAN	P50332 xenopus lae
5	178	7.5	962	1 MYSN_ACACA	060763 homo sapien
6	176	7.4	1509	1 MISS_CIPCA	P0559 acanthamoeb
7	173.5	7.3	1935	1 MYH4_RABIT	Q90339 cyprinus ca
8	172	7.2	1938	1 MYH2_DICDI	Q28041 oryctolagus
9	172	7.2	2116	1 RAS50_RQUAE	P08799 dictyosteli
10	170	7.1	978	1 TANA_XENLA	067124 aquifer aeo
11	169.5	7.1	1744	1 MYH3_RAT	Q01550 xenopus lae
12	169.5	7.1	1940	1 MYH7_RAT	P12847 rattus norv
13	169	7.1	1935	1 VDP_MOUSE	P02664 rattus norv
14	168	7.0	941	1 PAM_STRPY	Q9zzz2 mus musculu
15	168	7.0	1325	1 G160_MOUSE	P55937 mus musculu
16	168	7.0	1941	1 MH2_HUMAN	Q9uhx2 homo sapien
17	167	7.0	879	1 MYS_P_ONCVO	Q02171 onchocerca
18	167	7.0	880	1 MYS_P_BRUMA	Q00202 brugia mala
19	167	7.0	2411	1 MSA_DROME	P05661 drosophila
20	166	7.0	388	1 PAM_STRPY	P49054 streptococc
21	166	7.0	959	1 VDP_RAT	P41542 rattus norv
22	155	7.0	1935	1 MH7_PIG	P79393 sus scrofa
23	166	7.0	1939	1 MYH1_HUMAN	P12882 homo sapien
24	166	7.0	1960	1 MYH9_HUMAN	P3579 homo sapien
25	166	7.0	2704	1 BPAL_HUMAN	Q03001 homo sapien
26	165.5	6.9	1790	1 USP1_YEAST	P25386 saccharomy
27	165	6.9	848	1 MYS_P_DIRIM	P13392 dirofilaria
28	165	6.9	886	1 RA50_ARCFU	Q92330 archaeoglob
29	164.5	6.9	880	1 RA50_PYRAB	Q9uc8 pyrococcus
30	163.5	6.9	483	1 M6_STRPY	P08089 streptococc
31	163.5	6.9	1453	1 Y373_BOVIN	Q9tl23 bos taurus
32	163.5	6.9	1639	1 LMG1_DRONE	P15115 drosophila
33	6.9			1 ALML_SCHPO	Q9utk5 schizosacch

## ALIGNMENTS

34	163.5	6.9	1976	1 MYHA_HUMAN	P235580 homo sapien
35	163.5	6.9	2871	1 DESP_HUMAN	P12883 homo sapien
36	163	6.8	1935	1 MYH7_HUMAN	P13538 gallus gall
37	163	6.8	1938	1 MYSF_CHICK	Q95239 homo sapien
38	162.5	6.8	1232	1 KF4A_HUMAN	P24733 aequipinn
39	162.5	6.8	1938	1 MYS_A_EQIR	Q99966 h a-kinase
40	162.5	6.8	3911	1 AKAP_HUMAN	P33176 homo sapien
41	162	6.8	963	1 KINH_HUMAN	P02566 caenorhabdi
42	152	6.8	1965	1 MYSB_CAEEL	Q9f623 homo sapien
43	161.5	6.8	1939	1 MYHA_HUMAN	P12844 caenorhabdi
44	161.5	6.8	1969	1 MYS_A_EQEL	Q98638 mus musculus
45	161.5	6.8	1972	1 MYH2_MOUSE	

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Db	114	RNATVVSQALGKAEMCSTIKKQVKYLEQQDET--KQAQEAG--RLRKMTT	165
Db	1681	MR-SVTKBRDRSVE--ETKVERDOLKENRETTIRDLKEQEEKVHMLIKEOET	1736
Db	1563	AVKRRLSTERESEILQNSRLADLEYHKSOVESELRSKUKLASTTEELQALNERSLTT	1622
Db	1777	IDKLRGIVSEKTBISNMQKDLHSNDALKAQDKLQIPEERLAHMHLKEQETIDKURGI	1796
Db	218	SGEVADKL---RKDFESSRSLQTVYSELQAKLELSAQDKLQSADR--EIMSLKK-	270
Db	1797	VSEKTDKLNSMOKDLENSNAKLOEKTQELKANEHOLITLKKDVNETOKVSEMEOKKQI	1856
Db	271	-----LTMQL-ETLNLPVPASETVDRL---VLESAPAVEVNLUKJRRPSFRDDI---	314
Db	1857	KDOSLTLSKLELENLNLAQELHENLEEMKSVKMERDNLRRVEETKLERDQLKESLQETK	1916
Db	315	-DINATEVDVTTPARPSSSH----GYEKIC-----EKSHPHQDYPK 355	355
Db	1917	ARDLEIQQELKT---ARMUSKEHETVDKLRKSEKTIQISDQDJKSKDQL---RK	1971
Qy	356	ICKGPRKESQL 366	
Qy	1972	: :     1972 IOELQKKELQL 1982	
RESULT	3		
YD86_SCBPO		STANDARD;	PRT; 1957 AA.
AC	010411;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	01-OCT-1996 (Rel. 34, Last annotation update)		
DE	Hypothetical protein 222.8 kDa Protein Cif3.06C in chromosome 1.		
GN	SPAC1F3_06C.		
OS	Schizosaccharomyces pombe (Fission yeast).		
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;		
OC	Schizosaccharomycetales; Schizosaccharomycetaceae;		
OC	Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;		
OC	Xenopoda; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;		
OX	NCBI_TaxID:8355;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Hirano T., Michison T.J.;		
RT	"A heterodimeric coiled-coil protein required for mitotic chromosome condensation in vitro." Cell 79:449-458 (1994).		
RL			
CC	-I- FUNCTION: REQUIRED FOR BOTH ASSEMBLY AND STRUCTURAL MAINTENANCE OF MITOTIC CHROMOSOMES.		
CC	-I- SUBUNIT: ASSOCIATES WITH XCAP-E PROBABLY AS HETERO DIMER.		
CC	-I- SUBCELLULAR LOCATION: NUCLEAR. DURING CHROMOSOME ASSEMBLY IN MITOTIC EXTRACTS, XCAP-C/E WAS RECRUITED TO THE CHROMATIN AND FORMED A DISCRETE INTERNAL STRUCTURE WITHIN ASSEMBLED CHROMOSOMES.		
CC	-I- DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COILED-COIL REGIONS FLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-TERMINUS.		
CC	-I- SIMILARITY: BELONGS TO THE SMC FAMILY.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).		
CC			
DR	EMBL; U13673; AAA66679.1; -.		
KW	HYPOTHETICAL PROTEIN.		
KW	SEQUENCE 1957 AA; 222785 MW; 3F480CA06171D9DA CRC64;		
Qy	Query Match	7.7%: Score 183.5; DB 1; Length 1957;	
Qy	Best Local Similarity	21.9%; Pred. No. 0.05; Mismatches 68; Conservative Matches 76; Conservative Mismatches 68; Gaps 11; Indels 77;	
Db	1386	EDNOLATLKLNQDHLNEIRKEDVKEKESUJISUELSLNQRQRESSLDAKNE 1445	
Qy	130	-MIGSTLKQMKYLEQQQDETQKQEEAAGRRLSRKMTW-----EQEILL--LQSQLP 178	
Db	1446	HMLDDTSRKNSLMEKIESINSSLDKFSELASAVEKLGALQKHSESISLMMENIKSQLQ 1505	
Qy	179	EVEEMIRGQVGGSQSAVEOLAVYCVSLKEYEN-----LKEARR 216	
Db	1506	EAKERIQ---V DSTIQEDHETLHTASKNNGVKGKLNQDPSII RDSENTEBOLNNLEAKRS 1562	
RESULT	4		
XPC_XENLA		STANDARD;	PRT; 1290 AA.
ID	XPC_XENLA		
AC	P50532;		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	01-OCT-1996 (Rel. 34, Last annotation update)		
DE	Chromosome assembly protein XCAP-C.		
GN	XCAP-C.		
OS	xenopus laevis (African clawed frog).		
OC	Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;		
OC	Xenopoda; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;		
OX	NCBI_TaxID:8355;		
RN	[1]		
RP	MEDLINE:95042742; Pubmed=7954811;		
RA	Hirano T., Michison T.J.;		
RT	"A heterodimeric coiled-coil protein required for mitotic chromosome condensation in vitro." Cell 79:449-458 (1994).		
RL			
CC	-I- FUNCTION: REQUIRED FOR BOTH ASSEMBLY AND STRUCTURAL MAINTENANCE OF MITOTIC CHROMOSOMES.		
CC	-I- SUBUNIT: ASSOCIATES WITH XCAP-E PROBABLY AS HETERO DIMER.		
CC	-I- SUBCELLULAR LOCATION: NUCLEAR. DURING CHROMOSOME ASSEMBLY IN MITOTIC EXTRACTS, XCAP-C/E WAS RECRUITED TO THE CHROMATIN AND FORMED A DISCRETE INTERNAL STRUCTURE WITHIN ASSEMBLED CHROMOSOMES.		
CC	-I- DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COILED-COIL REGIONS FLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-TERMINUS.		
CC	-I- SIMILARITY: BELONGS TO THE SMC FAMILY.		
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CC			
DR	EMBL; U13673; AAA66679.1; -.		
DR	InterPro; IPR003405; SMC_C.		
DR	InterPro; IPR003395; SMC_N.		
DR	Pfam; PF02483; SMC_C; 1.		
DR	Pfam; PF02463; SMC_N; 1.		
KW	Mitosis; ATP-binding; coiled coil; Nuclear protein.		
FT	NP_BIND 107 114	ATP (POTENTIAL).	
FT	DOMAIN 264 594	COILED COIL (POTENTIAL).	
FT	DOMAIN 764 1027	COILED COIL (POTENTIAL).	
FT	DOMAIN 1094 1129	COILED COIL (POTENTIAL).	
FT	DOMAIN 1263 1290	COILED COIL (POTENTIAL).	
FT	DOMAIN 60 65	POLY-PRO.	
FT	DOMAIN 747 750	POLY-GLY.	
FT	DOMAIN 841 844	POLY-ALA.	
FT	DOMAIN 1196 1220	ALA/ASP-RICH (DA-BOX).	
SQ	SEQUENCE 1290 AA; 146988 MW; 2931249924FE90F6 CRC64;		
Query Match	7.7%: Score 182.5; DB 1; Length 1290;		





CC -!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.  
 CC -!- SIMILARITY: CONTAINS 1 IQ DOMAIN.

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DR EMBL; D89992; BAA2069.1; :-.  
 DR EMBL; D50476; BAA03069.1; :-.  
 DR EMBL; D43700; BAA07802.1; :-.  
 DR HSSP; P08799; IMMEDIATE.  
 DR InterPro; IPR000408; IO.  
 DR InterPro; IPR004009; Myosin\_N.  
 DR InterPro; IPR02928; Myosin\_tail.  
 DR InterPro; IPR01609; myosin\_head.  
 DR Pfam; PF00612; IQ; 1.  
 DR Pfam; PF02736; Myosin\_N; 1.  
 DR Pfam; PF01576; Myosin\_tail; 1.  
 DR PRIMUS; PR00193; MYOSINHEAVY.  
 DR PRODOM; PD000355; myosin\_head; 1.  
 DR SMART; SM00015; IQ; 1.  
 DR SMART; SM00242; MYS; 1.  
 DR PROSITE; PS50096; IO; 1.  
 KW Myosin: Muscle protein; Coiled coil; Thick filament; Actin-binding; ATP-binding; Methylation; Alkylation; Calmodulin-binding; Multigene family.  
 FT DOMAIN 1 781 MYOSIN HEAD-LIKE.  
 FT DOMAIN 782 811 IQ.  
 FT DOMAIN 812 839 HINGE.  
 FT DOMAIN 840 1935 COILED COIL (POTENTIAL).  
 FT NP-BIND 178 185 ATP (POTENTIAL).  
 FT DOMAIN 659 681 ACTIN-BINDING.  
 FT DOMAIN 761 775 ACTIN-BINDING.  
 FT MOD\_RES 129 129 METHYLATION (TRI-) (POTENTIAL).  
 FT MOD\_RES 699 699 ALKYRATION (SH-2).  
 FT SEQUENCE 709 1935 AA: 221599 MW: 911244B67D63C83B CRG64;

Query Match 7.3%; Score 173.5; DB 1; Length 1935;  
 Best Local Similarity 22.3%; Pred. No. 0.16; Matches 72; Conservative 66; Mismatches 126; Indels 59; Gaps 11;

QY 31 LQCLIQSFETAPSPRCPPQRQVKGRTINKFLPDLAQEEVNIDREF----- 78  
 DR 1144 LEETSERLEBAGGATAAQIEMKKRKEAFQKMRDL--EESTLQHETAAIRKEQADS 1200  
 QY 79 --LKENELVNVRAGLSOKKEKUDSOVITDTLRTOLEERNATVSLQALGKALMESTL 135  
 DR 1201 VAEGLGEQIDNLRVYRKOLEKEKSYKMEIDDTSNE-----AVAKANLEKMCRL 1253  
 QY 136 KKQMKYLEQQDDEKIQQAQBEAGRURSKMT-----MEQIILLOSQLP----- 178  
 DR 1254 EDDOSEIKTKSDENVROENDMNQHQARLQETENGEBFSRQEELKALV-SQLTRQKQAVHQ 1312  
 QY 179 -----EVEMRIMVGVSOSAVOLAVYCVSLRKEYENLKEARRASGEVADKIRDFSS 232  
 DR 1313 IEELKURHLEEVVKAKNALAHAVOSARHCDLRLRQEIEERQEARLQRMGSKANSEVAQW 1372  
 QY 233 RSKLQT----VYSELDOAKLELSSAQOKDQSAKEIMSIIKKITMLOQTPLNIFPVASSTV 288  
 DR 1373 RTKYEIATQRTFEELEBAAKKL-AOR-LQDAESEIEAVNSKCAASLEKIKQ-RLOGEVE 1427  
 DR 289 DRLV-LESPAPVPEVNLKLRPST 310  
 DR 1428 DLMDIVERANSLAANLDKORNF 1450

CC RESULT 8  
 ID MYH4\_RABBIT STANDARD; PRT; 1938 AA.  
 ID MYH4\_RABBIT DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 AC Q28441; DT 16-OCT-2001 (Rel. 40, Created)  
 RA Wittlingerhofer A.; DE Myosin heavy chain, skeletal muscle, Juvenile.  
 RA Maeda K., Hosinova E., Roesch-Kleinlauf A., Schuster H., Gasperik J., OS Eryctolagus cuniculus (Rabbit).  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagidae; OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagidae; NCBI\_TaxID=9966; RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NEW ZEALAND WHITE; TISSUE=Skeletal muscle;  
 RA Wittlingerhofer A.; DR Submitted (Aug-1995) to the EMBL/GenBank/DDBJ databases.  
 RT Isolation, sequencing of myosin heavy chain cDNA from rabbit skeletal muscle and a novel cosynthesis of S-1 fragment with the essential and regulatory light chains.;  
 RT "Isolation, sequencing of myosin heavy chain cDNA from rabbit skeletal muscle and a novel cosynthesis of S-1 fragment with the essential and regulatory light chains.";  
 CC -!- FUNCTION: MUSCLE CONTRACTION  
 CC -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)  
 CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).  
 CC -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.  
 CC -!- DOMAIN: THE ROD-LIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,  
 CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.  
 CC -!- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATTER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (SI) AND 1 ROD-SHAPED SUBFRAGMENT (S2).  
 CC -!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.  
 CC -!- SIMILARITY: CONTAINS 1 IQ DOMAIN.

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CC RESULT 8  
 ID EMBL; U32574; AAA74199.1; :-.  
 DR HSSP; P08799; IMMEDIATE.  
 DR InterPro; IPR000408; IO.  
 DR InterPro; IPR04009; Myosin\_N.  
 DR InterPro; IPR02928; Myosin\_tail.  
 DR InterPro; IPR01609; myosin\_head.  
 DR Pfam; PF00612; IQ; 2.  
 DR Pfam; PF00063; myosin\_head; 1.  
 DR Pfam; PF02736; Myosin\_N; 1.  
 DR Pfam; PF01576; Myosin\_tail; 1.  
 DR PRIMUS; PR00193; MYOSINHEAVY.  
 DR PRODOM; PD000355; myosin\_head; 1.  
 DR SMART; SM00015; IQ; 1.  
 DR SMART; SM00242; MYS; 1.  
 DR PROSITE; PS50096; IO; 1.  
 KW Myosin: Muscle protein; Coiled coil; Thick filament; Actin-binding; Calmodulin-binding; ATP-binding; Methylation; Alkylation; Multigene family.  
 KW MYOSIN HEAD-LIKE.  
 FT DOMAIN 1 783 IQ.  
 FT DOMAIN 784 813 COILED COIL (POTENTIAL).  
 FT NP-BIND 842 1938 ATP (POTENTIAL).  
 FT DOMAIN 842 1938 COILED COIL (POTENTIAL).  
 FT NP-BIND 179 186 ATP (POTENTIAL).  
 FT DOMAIN 658 680 ACTIN-BINDING (BY SIMILARITY).  
 FT MOD\_RES 760 774 METHYLATION (MONO-) (BY SIMILARITY).  
 FT MOD\_RES 35 35 METHYLATION (TRI-) (BY SIMILARITY).  
 FT MOD\_RES 130 130 METHYLATION (TRI-) (BY SIMILARITY).  
 FT MOD\_RES 552 552 METHYLATION (TRI-) (BY SIMILARITY).  
 FT MOD\_RES 756 756 ALKYRATION (SH-1) (BY SIMILARITY).  
 FT MOD\_RES 698 698 ALKYRATION (SH-1) (BY SIMILARITY).

FT	MOD_RES	708	708	ALKYLATION (SH-2) (BY SIMILARITY).	RP	X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 1-762.
SQ	SEQUENCE	1938	AA;	223064 MW; D88AEC5B182626 CRC64;	RX	MEDLINE=95345066; PubMed=17975;
		Best Local Similarity	21.3%	Score 172; DB 1; Length 1938;	RA	Fisher A.J., Smith C.A., Thoden J.B., Smith R., Sutoh K., Holden H.M., Rayment I.;
		Matches	86;	Conservative 82; Mismatches 148; Indels 88; Gaps 16;	RT	x-ray structures of the myosin motor domain of Dictyostelium discoideum complexed with MgADP-Befx and MgADP-Alfa-.";
QY	31	LOCLIOSFETAPSRCPQCRIQWGRKRNINLFLFDLQAQEENVLDRBF-----	78		RL	Biochemistry 34:8960-8972(1995).
Db	1146	LBEISERLEAGGATSAQIEMMKRKEAFQKMRDL--EATLQHETATAATLKKHADS	1202		RN	[5]
QY	79	--LKNELDNYRAQLSQDKDQRDSQVILDLRDTLEERNATVSIQQALGKAMECSTL	135		RP	X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 1-762.
Db	1203	VAELEGQIDNLQRVKORKEKESLKLMMKRNKREAFQKMRDL--EATLQHETATAATLKKHADS	1255		RA	MEDLINE=95345067; PubMed=7619756;
QY	136	KKQMKYIEQQDEK-----QAESEAGRLL-----RSKMKTMEQI	169		RA	Smith C.A., Rayment I.;
Db	1256	EDQVSLEUKTKBEEHQRLINDLSAQARLQTESGEFSRQLDKEKDLSVSQLSRGKQATQOI	1315		RT	"X-ray structure of the magnesium(III)-pyrophosphate complex of the truncated head of Dictyostelium discoideum myosin to 2.7-A resolution.";
QY	170	EMLQLSQPEVEMIRDMGVQSASVOLAVCVSLKEYENNIKEARKASGEVADKLRLD	229		RL	Biochemistry 34:8973-8981(1995).
Db	1316	EELKR---QLEEEIKAKSALAHALOSARHPDCDLRQEYEQEAKAKLORAMSKANEV	1371		RN	[6]
QY	230	FSSRSKQT---WYSDQAKLELSAQDQSAKEIMSKKLMQEPNLNPVAS	285		RP	X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-762.
Db	1372	AQWRTKYETDQATTEEELAKKL-AQR-LQDAEERHVAVNKASCLEKTK-Q-RLQN	1426		RA	MEDLINE=96206189; PubMed=8611530;
QY	286	EWVDRLV-LESPAPVNEVLKLRRSPFRDDI-----DLNATFDVDTPPARPSSQ-	333		RA	Smith C.A., Rayment I.;
Db	1427	-----CLESKHSPIQ---DVRKICKGPKRKESQL	366		RT	"X-ray structure of the magnesium(II).ADP vanadate complex of the Dictyostelium discoideum myosin motor domain to 1.9-A resolution.";
QY	334	--HGYYEKL---CLEKSHPHQ---DVRKICKGPKRKESQL	366		RL	RT of the Dictyostelium discoideum myosin motor domain.";
Db	1486	KVVKNAVEESDQLETLKRENKLNQEQTSIDLQIAEGGKTHEL	1529		RN	Biochemistry 35:5404-5417(1996).
					RP	[7]
RESULT	9				RP	X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 1-762.
MS2_DICTDI		STANDARD;	PRT;	2116 AA.	RX	MEDLINE=97452580; PubMed=9305951;
ID					RA	Gulick A.M., Bauer C.B., Thoden J.B., Rayment I.;
AC					RT	"X-ray structure of the MgADP, MgATPgammaS, and MgAMPNP complexes of the Dictyostelium discoideum myosin motor domain.";
DT	01-NOV-1988	(Rel. 09, Created)			RL	Biochemistry 36:11619-11628(1997).
DT	01-OCT-1989	(Rel. 12, Last sequence update)			RN	[8]
DT	16-OCT-2001	(Rel. 40, Last annotation update)			RP	X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-762.
DE	Myosin II heavy chain, non muscle.				RX	MEDLINE=98070605; PubMed=9401548;
GN	MyCA.				RA	Bauer C.B., Kuhiman P.A., Bagshaw C.R., Rayment I.;
OS	Dictyostelium discoideum (Slime mold).				RT	"X-ray crystal structure and solution fluorescence characterization of Mg2+(3')-O-(N-methylanthraniloyl) nucleotides bound to the Dictyostelium discoideum myosin motor domain.";
OC	Dicyostelium discoideum (Slime mold); Myctozoa; Dictyosteliida; Dictyostelium.				RL	J. Mol. Biol. 274:394-407(1997).
OX	NCBI_TAXID=44689;				CC	- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN & HAS ATPASE ACTIVITY THAT IS ACTIVATED BY ACTIN.
RN	[1]	SEQUENCE FROM N.A. MEDLINE=87032266; PubMed=3540939;			CC	- SUBUNIT: MYOSIN II HEAVY CHAIN IS TWO-HEADED. IT SELF-ASSEMBLES INTO FILAMENTS. HEXAMER OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
RP	Warrick H.M., de Lozanne A., Leinwand L.A., Spudich J.A. "Conserved protein domains in a myosin heavy chain gene from Dictyostelium discoideum.", Proc. Natl. Acad. Sci. U.S.A. 83:9433-9437(1986).			CC	- SUBCELLULAR LOCATION: HIGHEST CONCENTRATION IN THE POSTERIOR CELL CORTEX.	
RC	[2]	PHOSPHORYLATION SITES, AND MUTAGENESIS.			CC	- DOMAIN: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN BE FURTHER SPLIT INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).
RC	STRAIN-AX2;				CC	- DOMAIN: THE ROD-LIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
RP	Lueck-Vielmetter D., Schleicher M., Grabatin B., Wippler J., Raier G.; "Replacement of threonine residues by serine and alanine in a phosphorylatable heavy chain fragment of Dictyostelium myosin II.", FEBS Lett. 269:239-243(1990).			CC	- PTM: PHOSPHORYLATION INHIBITS THICK FILAMENT FORMATION AND REDUCES THE ACTIN-ACTIVATED ATPASE ACTIVITY.	
RX	PHOSPHORYLATION SITES.				CC	- MISCELLANEOUS: DICTYOSTELIUM MYOSIN II HAS NO K(2)EMPAT ATPASE ACTIVITY, PERHAPS CORRELATED WITH THE ABSENCE OF A CYS AT THE SH-1 POSITION (688).
RX	MEDLINE=9033583; PubMed=2287408;				CC	- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
RX	Wagle G., Noegel A., Scheel J., Gerisch G.; "Phosphorylation of threonine residues on cloned fragments of the Dictyostelium myosin heavy chain.", FEBS Lett. 227:71-75(1988).			CC	- SIMILARITY: CONTAINS 1 IQ DOMAIN.	
RX	MEDLINE=8811226; PubMed=2828113;				CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
RX	Wagle G., Noegel A., Scheel J., Gerisch G.; "Phosphorylation of threonine residues on cloned fragments of the Dictyostelium myosin heavy chain.", FEBS Lett. 227:71-75(1988).				CC	[4]
DR	EMBL; M14628; AAA33227.1; -.				DR	
DR	A26655; A26655.				DR	
DR	S00250; S00250.				DR	
DR	IMMA; 03-DEC-97.				PDB	
DR	PDB; 1IMD; 17-AUG-96.				PDB	

				OC	Bacteria; Aquificales; Aquificaceae; Aquifex.
PDB;	1MMG;	03-DEC-97.		NCBI_Taxid=63363;	
PDB;	IMNN;	03-DEC-97.		OX	
PDB;	1MDN;	17-AUG-96.	[1]	RN	
PDB;	1MNE;	17-AUG-96.		RP	
PDB;	1VOM;	23-DEC-96.		RC	
PDB;	1LVK;	28-JAN-98.		STRAIN=VF5;	
DICTYDB;	DD01008;	mhcA.		MEDLINE=98196666; Pubmed=9537320;	
DR	InterPro;	IPR00048; IQ.		RA	
DR	InterPro;	IPR04009; myosin_N.		RA	
DR	InterPro;	IPR00160; myosin_head.		RA	
DR	Pfam;	PF00612; IQ; 2.		RA	Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
DR	Pfam;	PF0063; myosin_head; 1.		RT	Decker G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
DR	Pfam;	PF02736; Myosin_N; 1.		RT	"The complete genome of the hyperthermophilic bacterium Aquifex aeolicus";
KW	Myosin; Coiled coil; Actin-binding; ATP-binding; 3D-structure; Calmodulin-binding; Methylation; Alkylation; Phosphorylation.			RL	Nature 392:353-358 (1998).
FT	DOMAIN 1 761 791	MYOSIN HEAD-LIKE.		CC	-!- FUNCTION: Involved in DNA double-strand break repair (DSBR). The rad50/mre11 complex possesses single-strand endonuclease activity and ATP-dependent double-strand specific exonuclease activity.
FT	DOMAIN 817 2116	COILED COIL (POTENTIAL).		CC	Rad50 provides an ATP-dependent control of mre11 by unwinding and/or repositioning DNA ends into the mre11 active site (By similarity).
FT	NP_BIND 179 186	ATP.		CC	-!- SUBUNIT: Forms a complex with mre11 (By similarity).
FT	DOMAIN 638 660	ACTIN-BINDING.		CC	-!- SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
FT	DOMAIN 738 752	ACTION-BINDING.		CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/annotation">http://www.isb-sib.ch/annotation</a> or send an email to license@isb-sib.ch).
FT	MOD_RES 130 130	METHYLATION (DT <sup>-</sup> ) (POTENTIAL).		CC	DR
FT	MOD_RES 678 678	ALKYLATION (SH <sup>-1</sup> ).		CC	EMBL; AE000718; AAC07092; 1.
FT	MOD_RES 1823 1823	PHOSPHORYLATION (BY MHCK).		CC	InterPro; IPR00439; ABC transporter.
FT	MOD_RES 1833 1833	PHOSPHORYLATION (BY MHCK).		CC	DR
FT	MOD_RES 2029 2029	PHOSPHORYLATION (BY MHCK).		CC	AE000718; AAC07092; 1.
SQ	SEQUENCE 2116 AA; 243871 MW; 2FC3770BB1FB56A1 CRC64;			FT	DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete proteome.
				FT	NP_BIND 32 39
				FT	DNA repair; Hydrolase; ATP-binding; Coiled coil (POTENTIAL).
				FT	DOMAIN 160 826
				FT	COILED COIL (POTENTIAL).
				SQ	SEQUENCE 978 AA; 115897 MW; 9B0F2BF51ADD151 CRC64;
Query Match	7.2%	Score 172; DB 1; Length 2116;			
Best Local Similarity	27.4%	Pred No. 0; 2; Mismatches 49; Indels 109; Gaps 80; Gaps 17;			
Matches	90;	Conservative			
Db	852	DKLERSLKDTESNVYLDLQLQKAKETKLKAMYDSKDALSAQKRELEIRYEDMESELDEKK	911		
Qy	116	ATVVLSQLQALGKAEMLCSTLKQMKYLEGQODDETQQAQEGRURSKMKTMEQTELLQS	175		
Db	912	LALENLQNQKRSVE-----EVKRDLEELQSE-----QLRNLTLEKLKK	951		
Qy	176	OLPEVEEMIRDMVGQOS-AVEOLAVYCVCVSKKEKENLKAARKASGEVAKR--LARDLFS	232		
Db	952	YEERBLEEMKR-VNGQSDTSITSLRKIKDELQKEVELTQS-FSBESKRGVLEK----T	1004		
Qy	233	RSKLQTQVSELDQAKLELKSQAKDLSAQAKEMSLKKLQTMQETLNLPVASETVDRLL	292		
Db	1005	RVRQLQ--SELDDLTVRLIDSETKSSELLRQKKLKEELVKOVAL---AAEAAKLA	1056		
Qy	293	LESPAPVENVNLKURRPSEFDIDINATEFDVTPARPSSQHGYEKLGLEKSIPIQDV	352		
Db	1057	QEA-----ANKLQ---GEYTTELNEKFNSEV-TARSN-----VEKSKKTL-- 1092			
Qy	353	PKICKGPRKESOLSLGGSCAGEPDE	380		
Db	1093	-----ESQI-----VAVNNEBLDEE	1106		
RESULT	10				
RA50_AQAE	STANDARD;	PRT:	978 AA.		
ID	RA50_AQAE				
AC	AC_067124;				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Probable DNA double-strand break repair rad50 Atpase.				
GN	RAD50 OR AQ_1006.				
OS	aerobic.				
RESULT	11				
TANA_XENLA	STANDARD;	PRT:	1744 AA.		
ID	TANA_XENLA				
AC	AC_001550;				
DT	01-JUN-1994 (Rel. 29, Last sequence update)				
DT	01-JUN-1994 (Rel. 29, Last annotation update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				

DE Tanabin.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;  
 OC Xenopodinae; Xenopus.

OX NCBI\_TAXID=8355;  
 RN [1] - SEQUENCE FROM N.A.  
 RP TISSUE="tracheal head";  
 RX MEDLINE=92398961; PubMed=1524825;  
 RA Heimati-Brivanlou A.; Mann R.W.; Harland R.M.;  
 RT "A protein expressed in the growth cones of embryonic vertebrate  
 neurons defines a new class of intermediate filament protein.";  
 RL Neuron 9:417-428(1992).  
 CC -!- TISSUE SPECIFICITY: GROWTH CONES OF EMBRYONIC VERTEBRATE NEURONS.  
 CC -!- DEVELOPMENTAL STAGE: IS EXPRESSED IN THE NEURULA AND PERSIST  
 CC DURING EMBRYOGENESIS IN THE BRAIN, CRANIAL NERVES, AND SPINAL  
 CC CORD.  
 CC -!- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.  
 CC  
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 or send an email to license@isb-sib.ch).  
 CC  
 EMBL; M99387; AAAA9966.1; -.  
 DR PIR; JH0720; JH0720.  
 DR InterPro; IPR001644; IF.  
 DR Pfam; PF00038; filament; 2.  
 DR PROSITE; PS00226; IF; 1.  
 KW Intermediate filament; Coiled coil; Neurone.  
 FT DOMAIN 1 12 HEAD.  
 FT DOMAIN 13 314 ROD.  
 FT DOMAIN 315 1744 TAIL.  
 FT DOMAIN 8 48 COIL 1A.  
 FT DOMAIN 49 60 LINER 1.  
 FT DOMAIN 61 156 COIL 1B.  
 FT DOMAIN 157 179 LINER 12.  
 FT DOMAIN 180 193 COIL 2A.  
 FT DOMAIN 194 199 LINER 2.  
 FT DOMAIN 200 314 COIL 2B.  
 SQ 1744 AA; 199561 MW; 6502EAC9FEB6C4E93 CRC64;

Query Match 7.1%; Score 169.5; DB 1; Length 1744;  
 Best local Similarity 25.7%; Pred. No. 0.22; Mismatches 61; Conservative 53; MisMatches 74; Indels 39; Gaps 9;

Qy 67 AQDEBNVLDREFKLNEDVNRAQLSQDKEKRQSVIITDLRLEERNATVVSLSQQLIG 126  
 Db 33 ALEREEN---ELIRKEIMSLRSKSERWKKHHHEMM-KLRQALDDCHREMV----- 80

Qy 127 KAEMLCSTLKQKYLEQQDETQKAQAEAGRRLSKMKTMEQTELLSQL-----P 178  
 B1 QAEVNRDSYEELEFKVORKCQEADKELSEKLSKLEBTRAQIWLKERLGOLEA 140

Qy 179 EVEEMIRDGMVGGSAAVEOLAVIVCVSLKEYENIKEARKA-SGEVADKLRK-DLFSS-- 232  
 141 ELDIDLREEEAKALME---ETASFSQRLENTRVAPVAFPKPVDFYDKRKLSIWIQGAV 197

Qy 233 --RSKLQTVYSLEQSKAQLEKSAQKD-----LOSADKEIMSLKKLTQMLQETLN 279

Db 198 EEEKSEVSELEAGJLSESENKRNKYLEENKRNQNLQSLDKEVLSKMRKEALDDLS 254

RESULT 12  
 RATE MYH3 RAT STANDARD PRT; 1940 AA.  
 ID MYH3 RAT  
 AC P12847;  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Myosin heavy chain, fast skeletal muscle, embryonic.  
 DE Myf3.  
 OS Rattus norvegicus (Rat);  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TAXID=10116;  
 RN [1] - SEQUENCE FROM N.A.  
 RP TISSUE="tracheal head";  
 RX MEDLINE=87060988; PubMed=3783701;  
 RA Strehler E.E.; Strehler-Page M.-A.; Perriard J.C.; Periasamy M.,  
 Nadal-Ginard B.; "Complete nucleotide and encoded amino acid sequence of a mammalian  
 myosin heavy chain gene. Evidence against intron-dependent evolution  
 of the rod.";  
 RL J. Mol. Biol. 190:291-317(1986).  
 CC -!- FUNCTION: MUSCLE CONTRACTION.  
 CC -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2  
 CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)  
 CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).  
 CC -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.  
 CC -!- DOMAIN: THE ROD-LIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING  
 CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES.  
 CC -!- PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY  
 CC ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.  
 CC -!- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT  
 CC MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE  
 CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (SI) AND 1 ROD-SHAPED  
 CC SUBFRAGMENT (S2).  
 CC -!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.  
 CC  
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 or send an email to license@isb-sib.ch).  
 CC  
 EMBL; X04267; CAA27817.1; -.  
 DR PIR; A24922; A24922.  
 DR HSSP; P08799; IMND.  
 DR InterPro; IPR000409; IO.  
 DR InterPro; IPR000409; Myosin\_N.  
 DR InterPro; IPR002928; Myosin\_tail.  
 DR InterPro; IPR02017; Spectrin.  
 DR InterPro; IPR01609; myosin\_head.  
 DR Pfam; PF00612; IQ; 2.  
 DR Pfam; PF00063; myosin\_head; 1.  
 DR Pfam; PF02735; Myosin\_N; 1.  
 DR Pfam; PF01576; Myosin\_tail; 1.  
 DR PRINTS; PR00193; MYOSIN\_HEAVY.  
 DR PRODOM; PD000355; myosin\_head; 1.  
 DR SMART; SM00015; IQ; 1.  
 DR PROSITE; PS50995; IQ; 1.  
 DR Myosin; Muscle protein; Coiled coil; thick filament; Actin-binding;  
 KW Calmodulin-binding; ATP-binding; Methylation; Alkylation;  
 KW Calmodulin family.  
 FT DOMAIN 1 781 MYOSIN HEAD-LIKE.  
 FT DOMAIN 782 811 IO.  
 FT DOMAIN 840 1933 COILED COIL (POTENTIAL).  
 FT NP\_HIND 179 186 ATP (POTENTIAL).  
 FT DOMAIN 656 678 ACTIN-BINDING.  
 FT DOMAIN 758 772 ACTIN-BINDING.  
 FT MOD\_RES 130 130 METHYLATION (TIRR-) (POTENTIAL).  
 FT MOD\_RES 696 696 ALKYLATION (SH-1).  
 FT MOD\_RES 706 706 ALKYLATION (SH-2).  
 SQ 1940 AA; 223857 MW; B5D546A596E55A696 CRC64;



QY	136	KROMKYLEQQDETQKQEQEAGRRLRKMT-----MEDIELLQLSQLP-----	178
Db	1253	EDQNEHRSKABETORSVNDLQRQLQTENGELSRQLDEKEALI-SQLTRGKLTYTQ	1311
Qy	179	-----EVEMIRDMGVQGSQAVEQALAVYCVSUKKEVNLKARKASGEVADKLKOLFSS	232
Db	1312	LEDLKROLLEEKVKAKNALAHQSARHDCDILREPEEEAKELQRVISKANSEWAQN	1371
Qy	233	RSKLQT---VSELDOAKLKSQADKETMSKKLTMQET	277
Db	1372	RKVYEDAIQTEELBAAKKL-AQR-LQDDEAEVAVNAKCSSLKT	1417
RESULT	14	*	*
VDP_MOUSE		STANDARD;	PRT:
ID			941 AA.
AC	092120;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DE	General vesicular transport factor p115 (transcytosis associated protein) (TAP) (vesicle docking protein) (Fragment).		
GN	VDP.		
OS	MUS musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=129; TISSUE=Thymus;		
RA	Han S-J;		
RT	*Identification of mouse TAP (transcytosis associated protein/p115)."; Submitted (Oct-1998) to the EMBL/Genbank/DDBJ databases.		
RL			
CC	- I- FUNCTION: GENERAL VESICULAR TRANSPORT FACTOR REQUIRED FOR INTERCISTERINAL TRANSPORT IN THE GOLGI STACK. IT IS REQUIRED FOR TRANSCYTOTIC FUSION AND/OR SUBSEQUENT BONDING OF THE VESICLES TO THE TARGET MEMBRANE. MAY WELL ACT AS A VESICULAR ANCHOR BY INTERACTING WITH THE TARGET MEMBRANE AND HOLDING THE VESICULAR AND TARGET MEMBRANES IN PROXIMITY (BY SIMILARITY).		
CC	- I- SURCELLULAR LOCATION: PERIPHERAL MEMBRANE PROTEIN WHICH RECYCLES BETWEEN THE CYTOSOL AND THE GOLGI APPARATUS DURING INTERPHASE (BY SIMILARITY).		
CC	- I- DOMAIN: COMPOSED OF A GLOBULAR HEAD, AN ELONGATED TAIL (COILED-COIL) AND A HIGHLY ACIDIC C-TERMINAL DOMAIN.		
CC	- I- TM: PHOSPHORYLATED IN A CELL CYCLE-SPECIFIC MANNER; PHOSPHORYLATED IN INTERPHASE BUT NOT IN MITOTIC CELLS.		
CC	- I- DEPHOSPHORYLATED PROTEIN ASSOCIATES WITH THE GOLGI MEMBRANE; PHOSPHORYLATION PROMOTES DISSOCIATION (BY SIMILARITY).		
CC	- I- SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.		
CC	-----		
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CC	-----		
CC	DR	Interpro: IPRO00219; Rhogef.	
CC	DR	EMBL: AR096868; AAC72967.1; -	
CC	DR	MGI: 1929095; Vdp.	
CC	DR	Interpro: IPRO00245; Armadillo.	
CC	DR	SMART; SM0025; Rhogef, 1.	
CC	DR	PROSITE: PS50176; ARM_REPEAT; UNKNOWN_1.	
CC	KW	Phosphorylation.	
CC	NON_TER	1	
FT	DOMAIN	<1	619
FT	DOMAIN	620	912
FT	DOMAIN	917	941
FT	MOD_RES	922	942
SQ	SEQUENCE	941 AA;	105152 MW;
Db	136	KROMKYLEQQDETQKQEQEAGRRLRKMT-----MEDIELLQLSQLP-----	178
Db	1253	EDQNEHRSKABETORSVNDLQRQLQTENGELSRQLDEKEALI-SQLTRGKLTYTQ	1311
Qy	179	-----EVEMIRDMGVQGSQAVEQALAVYCVSUKKEVNLKARKASGEVADKLKOLFSS	232
Db	1312	LEDLKROLLEEKVKAKNALAHQSARHDCDILREPEEEAKELQRVISKANSEWAQN	1371
Qy	233	RSKLQT---VSELDOAKLKSQADKETMSKKLTMQET	277
Db	1372	RKVYEDAIQTEELBAAKKL-AQR-LQDDEAEVAVNAKCSSLKT	1417
RESULT	14	*	*
VDP_MOUSE		STANDARD;	PRT:
ID			941 AA.
AC	092120;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DE	General vesicular transport factor p115 (transcytosis associated protein) (TAP) (vesicle docking protein) (Fragment).		
GN	VDP.		
OS	MUS musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CD-1; TISSUE=Testis;		
RX	MEDLINE:97-217683; Pubmed=906364;		
RA	Kondo M., Satou S.;		
RT	"Cloning and molecular characterization of cDNA encoding a mouse male-enhanced antigen-2 (Mea-2): a putative family of the Golgi autoantigen,"		
RT	DNA Seq 7-71-82(1997).		
CC	- I- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN SPERMATOGENESIS AND/OR TESTIS DEVELOPMENT. PROBABLY IDENTICAL WITH THE SEROLOGICALLY DETECTABLE MALE ANTIGEN (SDM).		
CC	- I- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS. TRANSCRIPTS CAN BE FOUND IN SPERMATIDS DURING SPERMATOGENESIS. NO EXPRESSION IN LEYDIG CELLS, SPERMATOZOA, OR SPERMATOCTYES.		
CC	- I- SIMILARITY: HIGH, TO HUMAN GOLGIN-160.		
CC	- I- CAUTION: IT IS UNCERTAIN WHETHER MET-1, MET-19 OR MET-30 IS THE INITIATOR.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		



RESULT 17

MYSP\_ONCVO STANDARD; PRT; 879 AA.

ID MISP\_ONCVO AC 002171; DT 01-JUN-1994 (Rel. 29, Created)  
01-JUN-1994 (Rel. 29, Last sequence update)  
16-OCT-2001 (Rel. 40, Last annotation update)

DE Paramyosin.  
OS Onchocerca volvulus.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
OC Onchoecide; Onchocerca.  
OX NEBI\_TAXID=6282;

RN [1]

SEQUENCE FROM N.A.  
MEDLINE=93165084; PubMed=7679477;

RA Dahmen A., Gallin M., Schumacher M., Ertmann K.D.;  
RT "molecular cloning and pre-mRNA maturation of *Onchocerca volvulus* paramyosin.";  
RL Biochem. Parasitol. 57: 335-338(1993).

-!- FUNCTION: Paramyosin IS A MAJOR STRUCTURAL COMPONENT OF MANY THICK FILAMENTS ISOLATED FROM INVERTEBRATE MUSCLES.

-!- SUBUNIT: HOMODIMER (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.  
-!- SIMILARITY: HIGH, TO MYOSIN HEAVY CHAINS.

CC

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CC

EMBL; M95813; AAA29431.1; -.

DR HSSP; P80220; 1DIP.  
DR InterPro; IPR002028; Myosin-tail.  
DR Protein; P01576; Myosin\_tail\_1.

KW Coiled coil; Muscle protein; Thick filament; Myosin.

FT DOMAIN 1 36 NONHELCICAL REGION (POTENTIAL).  
FT DOMAIN 37 860 COILED COIL (POTENTIAL).

FT DOMAIN 861 879 NONHELCICAL REGION (POTENTIAL).  
SQ SEQUENCE 879 AA; 101125 MW; DCA24AC01A9F02B1 CRC64;

Query Match 7.0%; Score 167; DB 1; Length 879;  
Best Local Similarity 19.8%; Pred. No. 0..13; Mismatches 105; Conservative 19.8%; Indels 178; Gaps 20; Matches 160;

RESULT 18

MYSP\_BRUMA STANDARD; PRT; 880 AA.

ID MISP\_BRUMA AC 001202; P90711; DT 01-FEB-1996 (Rel. 33, Created)  
15-JUL-1998 (Rel. 36, Last sequence update)

DE Paramyosin.  
OS Brugia malayi.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
OC Onchoecide; Brugia.  
OX NEBI\_TAXID=6279;

RN [1]

SEQUENCE FROM N.A.  
Lang Y.S., Luquaud P., Nicolas L.;  
RL Submitted (NOV-1996) to the EMBL/GenBank/DDJB databases.

[2]

SEQUENCE OF 180-263 AND 684-880 FROM N.A.  
MEDLINE=9211068; PubMed=1775173;

RA Li B., Chandrasekar R., Alvarez R.M., Lifitis F., Weil G.J.;  
RT "Identification of paramyosin as a potential protective antigen against *Brugia malayi* infection in Jirds";  
RL Biochem. Parasitol. 49:315-324(1991).

-!- FUNCTION: Paramyosin IS A MAJOR STRUCTURAL COMPONENT OF MANY THICK FILAMENTS ISOLATED FROM INVERTEBRATE MUSCLES.

-!- SUBUNIT: HOMODIMER (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.  
-!- SIMILARITY: HIGH, TO MYOSIN HEAVY CHAINS.

CC

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CC

DR U77590; AAC18613.1; -.

DR M63097; AAC27859.1; -.

DR M63098; AAC27860.1; -.

DR HSSP; P80220; 1DIP.

DR InterPro; IPR002928; Myosin\_tail.  
 DR Pfam; PF01576; Myosin\_tail; 1.  
 KW Coiled coil; Muscle protein; Thick filament;  
 Myosin.  
 FT DOMAIN 1 34 NONHEICAL REGION (POTENTIAL).  
 FT DOMAIN 35 859 COILED COIL (POTENTIAL).  
 FT DOMAIN 860 880 NONHEICAL REGION (POTENTIAL).  
 FT CONFLICT 189 189 V -> I (IN REF. 2).  
 FT CONFLICT 197 197 D -> A (IN REF. 2).  
 FT CONFLICT 251 251 L -> F (IN REF. 2).  
 FT CONFLICT 255 255 E -> Q (IN REF. 2).  
 FT CONFLICT 696 696 A -> R (IN REF. 2).  
 FT CONFLICT 730 736 FRKUKR -> IOPETAA (IN REF. 2).  
 FT CONFLICT 825 825 L -> IQ (IN REF. 2).  
 FT CONFLICT 857 880 HOLLRAKMRQKTFPSKNSRDN -> SSVUTGKNASASK  
 FT SEQUENCE 880 AA; 101904 MW; F79A2)E642D4A85E CRC64;  
 SQ [3].

Query Match 7.0%; Score 167; DB 1; Length 880;  
 Best Local Similarity 19.6%; Pred. No. 0.13; Mismatches 20;  
 Matches 104; Conservative 89; Indels 178; Gaps 20;  
 Qy 59 INKLUFFDIAQE-----ENVREF--LKNELDN--VRAQISQSKDEKR----- 98  
 :::: |||| : | | | : | | | : | | | : | | | : | | |  
 198 LNRIVNDLAQQRQLQAENDLKEIHDKVQDNLQHVKIQIAAQOLEARRLEDAERE 257  
 CC 99 -----DSQWIDTDLRDTBURNATVSIQDGLA----- 128  
 Db 258 RSDIQQAQHLHQVQELDSYPTALDEEASAARAEAKRKLALANTEIQTWKSKFDTAVLHHE 317  
 Qy 129 --EMLCSTLKQMKYLEQQ--DETQKAQEENGRLSKMKM----- 166  
 :::: ||| : | | | : | | | : | | | : | | | : | | |  
 318 VEDLRKKMLQKQABYEEOIEIMLQKISOLEKARSQLOZEVENVILVLDLEKAONTITLERA 377  
 Qy 167 -EQTELLIQSQQPEVEEMTRDMGSVQ----- 207  
 :::: ||| : | | | : | | | : | | | : | | | : | | |  
 378 KEDQLETKVNLKVIDELTVELLAQAREARAALAEQKLKNLYEKAVQKEALEARENKL 437  
 Db 208 YENLKEARKASGEVADKLK-DIFSSR----- 243  
 :::: ||| : | | | : | | | : | | | : | | | : | | |  
 Db 438 QDDIHEAKERALANRKLUHELDLENARLAGEIBLQALKESAAARDENRAENRQLAEL 497  
 Qy 244 DONKLELKSQAKDQISADKEIMSLKKKJMLQETLNLPVASTPVDRU---VIESPARVE 300  
 :::: ||| : | | | : | | | : | | | : | | | : | | |  
 Db 498 QQLRIEM--ERILOKEKEBEMEALRNKMQF-----EIDRLTAALADAEARMK 541  
 Qy 301 VNLKLRSSFRDDI-DLRTFD-----WTPPARPSSQHGYEKOLEKSIQDVP 353  
 :::: ||| : | | | : | | | : | | | : | | | : | | |  
 Db 542 AEISRLKKYQAEIALEMTVDNLRNRAEQTQKIQSEQLIKIQAISLEDPQRQLQPTL 601  
 Qy 354 KKICKGPKRESQSLGGSCAGEPDEELVGAFPIFVRNALGQKQPKPRSESCKDV 413  
 :::: ||| : | | | : | | | : | | | : | | | : | | |  
 Db 602 DQYALQQRKVSAELBEC-----KVALDNAIRRKQAEDLEEN----- 643  
 Qy 414 RTGFDSLGSRTKFIQOPTDVMILPLPVKPKTKVORVVKTVHSLFQAKLD 464  
 :::: ||| : | | | : | | | : | | | : | | | : | | |  
 Db 644 -----GRI-----TDLVSVN---NNLTAKN- KLETELSTAQADLD 675  
 RESULT 19

MYSA\_DRONE STANDARD; PRT; 2411 AA.

ID MYSA\_DRONE STANDARD; PRT; 2411 AA.

AC P05661; 01-NOV-1988 (Rel. 09, Created)

DT 01-JUN-1994 (Rel. 29, last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Myosin heavy chain, muscle.

GN MHC.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydriidae; Drosophilidae; Drosophila.

DR SMART; SM0015; IQ; 1.

DR NCBI\_TaxID=7277;

DR RN [1].

DR RP SEQUENCE FROM N.A.

DR RX MEDLINE:89384556; PubMed=2506434;

DR RA George E. L.; Ober M.B.; Emerson C.P. Jr.; "Functional domains of the *Drosophila melanogaster* muscle myosin heavy-chain gene are encoded by alternatively spliced exons.";

DR RT Mol. Cell. Biol. 9:2957-2974(1989).

DR RL [2].

DR RP SEQUENCE OF 1-312 FROM N.A.

DR RX MEDLINE:87280141; PubMed=3038896;

DR RA Wassenberg D. R. II; Kronert W.A.; O'bonnell P.T.; Bernstein S.I.; "Analysis of the 5' end of the *Drosophila* muscle myosin heavy chain gene. Alternatively spliced transcripts initiate at a single site and intron locations are conserved compared to myosin genes of other organisms.";

DR RT J. Biol. Chem. 262:10741-10747(1987).

DR RN [3].

DR RP SEQUENCE OF 486-881 FROM N.A.

DR RC STRAIN=CANTON-S; TISSUE=Embryonic muscle;

DR RX MEDLINE:91330870; PubMed=1907912;

DR RA Kronert W.A.; Edwards K.A.; Roche E.S.; Wells L.; Bernstein S.I.; "Muscle specific accumulation of *Drosophila* myosin heavy chains: a splicing mutation in an alternative exon results in an isoform."

DR RT EMBO J. 10:2479-2488(1991).

DR RL [4].

CC -|- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)  
 CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

CC -|- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

CC -|- ALTERNATIVE PRODUCTS: AS *DROSOPHILA* HAS A SINGLE MUSCLE MHC GENE, MHC ISOFORMS MUST RELY ON ALTERNATIVE RNA SPlicing THAT LEADS TO DIFFERENCES IN THE C-TERMINUS OF THE VARIOUS MHC PROTEINS.

CC -|- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LM) AND 1 HEAVY MEROMYOSIN (HM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).

CC -|- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

CC -|- SIMILARITY: CONTAINS 1 IQ DOMAIN.

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CC -----

DR EMBL; MG1229; AAA28686\_1; ALT\_SEQ.

DR EMBL; MG1229; AAA28687\_1; ALT\_SEQ.

DR EMBL; J02788; AAA28706\_1; ALT\_SEQ.

DR EMBL; J02788; AAA28707\_1; ALT\_SEQ.

DR EMBL; X60195; CAA2752\_1; ALT\_SEQ.

DR EMBL; X60196; CAA2753\_1; ALT\_SEQ.

DR EMBL; X60196; CAA42754\_1; ALT\_SEQ.

DR PIR; A2892; A2892.

DR PIR; A32491; A32491.

DR PIR; A32491; A32491.

DR HSP; P08799; 1MD.

DR FlyBase; FBgn00241; Mhc.

DR InterPro; IPR000048; IQ.

DR InterPro; IPR04009; Myosin\_N.

DR InterPro; IPR02928; Myosin\_tail.

DR InterPro; IPR001609; myosin\_head.

DR Pfam; PF00612; IQ; 2.

DR Pfam; PF00053; myosin\_head; 7.

DR Pfam; PF02736; Myosin\_N; 1.

DR Pfam; PF01576; Myosin\_tail; 1.

DR PRINTS; PR00193; MYOSINHEAVY.

DR PRODOM; PD000355; myosin\_head; 5.

DR SMART; SM00242; IQ; 1.



RESULT 21						
VDP_RAT	STANDARD:	PRT:	959 AA.			
ID P41542; P-1542;				Query Match	7.0%	Score 166; DB 1; Length 959;
AC				Best Local Similarity	20.2%	Pred. No. 0.16; Gaps 11;
DT 01-NOV-1995 (Rel. 32, Created)				Matches	76; Conservative	Mismatches 93; Indels 152; Gaps 11;
DT 01-NOV-1995 (Rel. 32, Last sequence update)				QY 52	QVKRTTINKLFF-----DLAQEEENVLDRFLK-NELDNV-RQLS 91	
DE 16-OCT-2001 (Rel. 40, Last annotation update)				DE ::	:   :          :             :	
DE General vesicular transport factor p115 (transcytosis associated protein) (TAP) (vesicle docking protein).				Db 571	RIGKENYIEFKLGPIKHLYSRASQKPOPNFSPPEYMFIDHFRFTKLKYLSCVITKAIVY 630	
GN VDP.				QY 92	OKUEKEKRDSQVITDLRDLTEERNATVVSQOALGKAEMLCSTLKKOMYEQQDE-- 148	
OS Rattus norvegicus (Rat).				DB 631	SSEEDKKEEEV---KKTLEQHDNTVTHYKNIREQDQLEELKQVSTLKQNEQLOQ 685	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				QY 149	--TKQAO-----EAGRLASKMKTMEQI 169	
NCI_TAXID=1016; [1]				DB 686	AVIQOQASO1QOHKDQYNNLLKVQLGKDNNHHQGHSHDGAQVNGIOPPEISRLREIEELRH 745	
RC TISSUE-liver;				QY 170	EULLQSOLPVEEMIRM-----GVQOSAV-----EQLAV----- 200	
RX MEDLINE=9512633; PubMed=7031323;				DB 746	QVLIQSOLEAKDVIENLRSQVSGMSBQALATCSPRDAEQVAELKOLSOLCSOS 805	
RA Waters M.G.;				QY 201	-----CVSLKEYENLKBARK 216	
RA Barroso M., Nelson D.S., Szalai E.;				DB 806	LEITRLQPTENSELQQRNETLAKNSPVGESELVTAAKTIVDEGRILSALLQETKLNK 865	
RT 'transcytosis-associated protein (TAP)/p115 is a general fusion endoplasmic reticulum to Golgi transport factor required for binding of vesicles to acceptor membranes.';				QY 217	ASGEVADKLRLDFSSRSKLOTVYSELDAKLELSKQD-----LQADKEIMSLK 269	
RT factor required for binding of vesicles to acceptor membranes.';				DB 866	ALSEERTAIOKQOLDSSNSTTIAQTERDKLYLEVTDISKKEQDDLLVILLAODQKILSKS 925	
RL Proc. Natl. Acad. Sci. U.S.A. 92:522-526(1995).				QY 270	KUTMLQETLNLNPVASE 286	
CC -i- FUNCTION: GENERAL VESICULAR TRANSPORT FACTOR REQUIRED FOR INTERCISTERNA TRANSPORT IN THE GOLGI STACK. IT IS REQUIRED FOR TRANSCYTOTIC FUSION AND/OR SUBSEQUENT BINDING OF THE VESICLES TO THE TARGET MEMBRANE. MAY WELL ACT AS A VESICULAR ANCHOR BY INTERACTING WITH THE TARGET MEMBRANE AND HOLDING THE VESICULAR AND TARGET MEMBRANES IN PROXIMITY.				DB 926	KLKDIGH----PVEEE 937	
CC AND TARGET MEMBRANE WITH TWO N-TERMINAL HEADS AND A C-TERMINAL COILED-COIL TAIL. DIMER FORMED BY PARALLEL ASSOCIATION OF THE TAILS.				RN [1]	MYH7_PIG	
CC -!- SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE PROTEIN WHICH RECYCLES BETWEEN THE CYTOSOL AND THE GOLGI APPARATUS DURING INTERPHASE.				ID MYH7_PIG	STANDARD:	PRT; 1935 AA.
CC -!- DOMAIN: COMPOSED OF A GLOBULAR HEAD, AN ELONGATED TAIL (COILED-COIL), AND A HIGHLY ACIDIC C-TERMINAL DOMAIN.				AC P79293;		
CC -!- PTM: PHOSPHORYLATED IN A CELL CYCLE-SPECIFIC MANNER;				DT 15-DEC-1998 (Rel. 37, Created)		
CC PHOSPHORYLATED IN INTERPHASE BUT NOT IN MITOTIC CELLS;				DT 15-DEC-1998 (Rel. 37, Last sequence update)		
CC DEPHOSPHORYLATED PROTEIN ASSOCIATES WITH THE GOLGI MEMBRANE;				DT 16-OCT-2001 (Rel. 40, Last annotation update)		
CC PHOSPHORYLATION PROMOTES DISSOCIATION (BY SIMILARITY).				DE MYosin heavy chain, cardiac muscle beta isoform (MyHC-beta).		
CC -!- SIMILARITY: BELONGS TO THE VDP/MSO1/YH047C FAMILY.				GN MYH7.		
CC				OS Su scrofa (Pig).		
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).				OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
CC				OC NCBI_TaxID=9823;		
CC RN [1]				RN [1]	SEQUENCE FROM N.A.	
CC RP STRAIN-DOMESTICA;				RA Ko Y.L.;		
CC RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.				CC -!- FUNCTION: MUSCLE CONTRACTION.		
CC -!- SUSUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).				CC -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.		
CC -!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.				CC -!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.		
DR PROSITE; PS50176; ARM_REPEAT; UNKNOWN_1.				CC -!- PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.		
DR Transport; Protein transport; Golgi stack; Membrane; Coiled coil; Phosphorylation.				CC -!- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (SI) AND 1 ROD-SHAPED SUBFRAGMENT (S2).		
FT DOMAIN 1 637 GLOBULAR HEAD.				CC -!- MISCELLANEOUS: THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATPASE.		
FT DOMAIN 638 930 COILED COIL (POTENTIAL).				CC -!- MYOSIN WHILE THE BETA ISOFORM IS A 'SLOW' ATPASE.		
FT DOMAIN 935 959 ASP(GLU-RICH (ACIDIC)).				CC -!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.		
FT MOD_RES 940 940 PHOSPHORYLATION (BY SIMILARITY).				CC -!- SIMILARITY: CONTAINS 1 TO DOMAIN.		
FT CONFLICT 591 591 S -> P (IN REF. 2).				CC		
FT CONFLICT 658 658 M -> V (IN REF. 2).						
FT CONFLICT 816 816 S -> R (IN REF. 2).						
FT CONFLICT 873 873 A -> S (IN REF. 2).						
SQ SEQUENCE 959 AA; 107162 MW; 356394B4BC7E003B CRC64;				CC This SWISS-PROT entry is copyright. It is produced through a collaboration		

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EMBL; 075316; AAB37320; 1; -.

DR HSP; P08799; 1; IQ.

DR InterPro; IPR00048; 1Q.

DR InterPro; IPR004009; Myosin\_N.

DR InterPro; IPR002028; Myosin\_tail.

DR InterPro; IPR001609; myosin\_head.

Pfam; PF00612; IQ; 2.

Pfam; PF00653; myosin\_head; 1.

Pfam; PF02756; Myosin\_N; 1.

Pfam; PF01576; Myosin\_tail; 1.

PRINTS; PRO0193; MYOSINHEAVY.

Prodom; PD00035; myosin\_head; 1.

SMART; SM00015; IQ; 1.

SMART; SM0042; MSC; 1.

PROSITE; PS50096; IQ; 1.

KW Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; ATP-binding; Methylation; Alkylation; Multigene family; Calmodulin-binding.

KW DOMAIN 1 780 MYOSIN HEAD-LIKE.

FT DOMAIN 781 810 IQ.

FT DOMAIN 839 1935 COILED COIL (POTENTIAL).

NP BIND 178 185 ATP (POTENTIAL).

DOMAIN 655 677 ACTIN-BINDING.

FT DOMAIN 757 771 ACTIN-BINDING.

FT MOD\_RES 129 129 METHYLATION (TRI-) (POTENTIAL).

FT MOD\_RES 695 695 ALKYLATION (SH 2) (POTENTIAL).

FT MOD\_RES 705 705 ALKYLATION (SH 2) (POTENTIAL).

SEQUENCE 1935 AA; 223110 MW; 149CDBFD910DBB08 CRC64;

Query Match 7.0%; Score 166; DB 1; Length 1935;

Best local Similarity 22.2%; Pred. No. 0..37; Matches 74; Conservative 62; Mismatches 131; Indels 66; Gaps 9;

Qy 79 LKNEILDNYRAQSLQSOKDKERKRSQDSVQIDPLRDTLEE---RNAYWVSSQQAAGKAEMCIST 134

Db 1287 LSQLDKEREALISQLQTRKLTYQQEDLRQLEEVAKNALAHALQSARAHADLREQ 1346

Qy 135 LKKOMVYLEQQDETQKQAEAGRRLSRMKT-----MEQTELLQSQQLPEVEEMRD 186

Db 1347 YEETETTAKELVRKSANSSEVAQWRTYEDAIORTEELEERAKKLAQRLODAEE--- 1402

Qy 187 MGVGOSAVEQALQYCVSKK-----EYENIK--EARAKSEGAVKLRKDFFSSK 236

Db 1403 -----AVERAANAKCSSELEKTTKHLQNIEDLAVERSNAAALDKQKRNFDKILAW 1456

Qy 237 QTVYSELDOQAKLILSAQKQDLSADKEIMSLKKRL-----TMLOBETLNQPPVABETV 288

Db 1457 KORYEE--SOSLESESSREARSLSTELFKKNAYEESLEHLETSKRENKNLQEESIDL 1513

Qy 289 DRUVLESAPPVENLKLRRPSFDDIDLNATEFLDVTPPARPSSQHGYYECKLEKSHSP 348

Db 1514 EOLGSSGKTHIELE-KVVRQLEAKELOS-----ALESEAS 1550

Qy 349 IQDPVKKCKGPKRKSQSLGGGSCAGPDEEL 381

Db 1551 LEHEEGKILRQAQLEFNQIKAMEMERKLAERKDEEM 1583

RESULT 23

MYHL\_HUMAN STANDARD: PRT; 1939 AA.

ID MYHL\_HUMAN STANDARD: PRT; 1939 AA.

AC P12882; Q9Y622; 1.

DT 01-OCT-1989 (Rel. 12, Created)

DT 16-OCT-2001 (Rel. 40, last sequence update)

DT 16-OCT-2001 (Rel. 40, last annotation update)

DE Myosin heavy chain, skeletal muscle, adult 1 (Myosin heavy chain DE T1x/d) (MyHC-IIx/d).

CC DE Tissue-Skeletal muscle; DE Tissue-Skeletal muscle;

CC GN MHC.

CC OS Homo sapiens (Human).

CC OC Embryo; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CC OC NCBI\_TAXID=9606;

CC RN [1]

CC RP Sequence from N.A.

CC RC Tissue-Skeletal muscle;

CC RX MEDLINE-99318869; Published=10388558;

CC RA Weiss A., Schiaffino S., Leinwand L.A.;

CC RT "Comparative sequence analysis of the complete human sarcomeric myosin heavy chain family: implications for functional diversity.";

CC RT J. Mol. Biol. 290:61-75(1999).

CC RN [2]

CC RP Sequence of 1064-1939 from N.A.

CC RX MEDLINE=86176778; PubMed=2421254;

CC RA Saez L., Leinwand L.A.;

CC RT "Characterization of diverse forms of myosin heavy chain expressed in adult human skeletal muscle";

CC RL Nucleic Acids Res. 14:2951-2969(1986).

CC RT -!!- FUNCTION: MUSCLE CONTRACTION.

CC CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

CC CC -!!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

CC CC -!!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

CC CC -!!- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

CC CC -!!- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).

CC CC -!!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

CC CC -!!- SIMILARITY: CONTAINS 1 IQ DOMAIN.

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CC DR EMBL; ART11785; AAD29951; 1; -.

CC DR EMBL; X03740; CAA27380; 1; -.

CC DR PIR; A23767; A23767.

CC DR HSP; P03437; 1HMT.

CC DR MM; 160730; -.

CC DR InterPro; IPR00048; 1Q.

CC DR InterPro; IPR002938; Myosin\_tail.

CC DR InterPro; IPR001609; myosin\_head.

CC DR Pfam; PF0063; myosin\_head; 1.

CC DR Pfam; PF01576; Myosin\_tail; 2.

CC DR PRINTS; PRO0193; MYOSINHEAVY.

CC DR Prodom; PD000355; myosin\_head; 1.

CC DR SMART; SM00015; myosin\_head; 1.

CC DR PROSITE; PS50096; IQ; 1.

CC KW Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; Calmodulin-binding; ATP-binding; Methylation; Alkylation; Multigene family.

CC FT DOMAIN 1 784 MYOSIN HEAD-LIKE.

CC FT DOMAIN 785 814 IQ.

CC FT DOMAIN 843 1939 COILED COIL (POTENTIAL).

CC FT DOMAIN 843 1939 COILED COIL (POTENTIAL).

CC FT DOMAIN 659 681 ACTIN BINDING (BY SIMILARITY).

CC FT DOMAIN 761 775 ACTIN-BINDING (BY SIMILARITY).

CC FT MOD\_RES 130 130 METHYLATION (TRI-) (POTENTIAL).

CC FT MOD\_RES 699 699 ALKYLATION (SH-1) (POTENTIAL).

FT MOD\_RES 709 709 ALKYLATION (SH-2) (POTENTIAL).  
 FT CONFLICT 1131 1131 A > T (IN REF. 2).  
 FT CONFLICT 1139 1139 C > T (IN REF. 2).  
 FT CONFLICT 1158 1158 G > V (IN REF. 2).  
 FT CONFLICT 1163 1163 A > T (IN REF. 2).  
 FT CONFLICT 1286 1289 TESG -> QMQV (IN REF. 2).  
 FT CONFLICT 1302 1303 VS -> ET (IN REF. 2).  
 FT CONFLICT 1451 1451 R -> T (IN REF. 2).  
 FT CONFLICT 1470 1470 E -> V (IN REF. 2).  
 FT CONFLICT 1473 1474 AS -> SF (IN REF. 2).  
 FT CONFLICT 1569 1569 L -> V (IN REF. 2).  
 FT CONFLICT 1598 1598 V -> E (IN REF. 2).  
 FT CONFLICT 1606 1606 D -> N (IN REF. 2).  
 FT CONFLICT 1643 1643 A -> D (IN REF. 2).  
 FT CONFLICT 1648 1648 R -> Q (IN REF. 2).  
 FT CONFLICT 1750 1750 O -> K (IN REF. 2).  
 FT CONFLICT 1822 1822 R -> K (IN REF. 2).  
 FT CONFLICT 1845 1845 R -> H (IN REF. 2).  
 SEQUENCE 1939 AA; 223114 MW; 39ADB26AB79DFA53 CRC64;

Query Match 7.0%; Score 16: DB 1; Length 1939;  
 Best Local Similarity 20.8%; Pred. No. 0.37%;  
 Matches 84; Conservative 83; Mismatches 149; Indels 88; Gaps 16;

Qy 31 LQCLIQSFTETAPSRCPCPQCRIQNGKRTIINKLFDLAQEENVLDERF----- 79  
 Db 1147 LEISERLEEEAGGAAATSAQTEMNKKREAFQKMRDL--EAEATLQHEATAATRKKHADS 1203

Qy 79 --LKNELDNVRQLSKOKKEKRDSQVITDTLROTLEERNATVVSQQLAGKALCSTL 135

Db 1204 VAELEGQIQLNQRYVKQKLKESEKMNKEDDLASNE-----TVSKAGKGNLEKMCRAL 1256

Qy 136 KKQMKYLEQQQDFTM-----QAOBEAGRL-----RSKNTMEOI 169

Db 1257 EDQSEIKTKEEQQORLINDTQARLOTESEGEYSRQLDEKKDTLVSQLSRGQAFTQI 1316

Qy 170 ELLIQSOLPEVEEMTRDMGVQGSQAVEQALAVYCSSLKKEYENLKEARKASGEVADKLKD 229

Db 1317 EELKR---OLEEEIKAKSALAHALQSSRHDCLIREQEEOEAKELQRAMSKANSEV 1372

Qy 230 FSSRSKLQT----WYSELDOQAKLKLQSKAQDKADEKMSLKKLTMQETNLNPYAS 285

Db 1373 AQWRKYTERDAIRTEELEEKKL---AQR-LDDEAHEVEAVNAVKCASILEKTQ---RQN 1427

Qy 286 ETVDRLV-LESPPAPEVNVKLRSPFRDDI-----DLNATFDVDTTPPARPSSQ-- 333

Db 1428 EVDLMIDVERTNACAAALDKKQRNF-DKILAEWKQKCBETHAABLEASOKESSLSLTF 1486

Qy 334 --HGYYEKL---CLEKSHSPTO---DVPKICKGPRKESQI 366

Db 1487 KIRKNAVEEESLDQIETLKRENKNIQQEISDLTEQIAEGGKRHIEL 1530

RESULT 24

MYH9\_HUMAN STANDARD; PRT; 1960 AA.

ID MYH9\_HUMAN ; STANDARD; PRT; 1960 AA.

AC P35579; 060805; [1]

DT 01-JUN-1994 (Rel. 29, Created)

DT 15-DEC-1998 (Rel. 37, last sequence update)

DE 01-MAR-2002 (Rel. 41, last annotation update)

DE Myosin heavy chain, nonmuscle myosin heavy chain, type A) (Nonmuscle myosin heavy chain A) (NMHC-A).

GN MYH9.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI\_TaxId=9606;

RN [1]

RP SEQUENCE FROM N.A.

RP MEDLINE-20057165; PubMed=10591208;

RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M., Clamp M., Smitk L.J., Ainscough R., Almeida J.P., Babbage A.,

RA Baguley C., Bailey J., Barlow K., Bates K.N., Beasley O., Bird C.P., Blakey S., Bridgeman A.M., Buck D., Burgess N.P., Burrill W.D., Burton J., Carter C., Carter N.P., Chen Y., Clark G., Clegg S.M., Cobley V., Cole C.G., Collier R.E., Connor R.E., Conroy D., Coryn N., Coville G.J., Cox A.V., Davis J., Dawson E., Dhani P.D., Docktree C., Dodsworth S.J., Durbin R.M., Ellington A., Evans K.L., Fey J.M., Fleming K., French L., Garner A.A., Gilbert J.G.R., Goward M.E., Graham D., Griffiths M.N., Hall C., Hall R., Hall-Taylor G., Hechtcott R.W., Ho S., Holmes S., Hunt S.E., Jones M.C., Kershaw J., Kimperley A., King A., Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M., Martyn I.D., Mashreghi-Mohammadi M., Matthews L., McCann O.T., McClay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J., Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J., Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T., Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L., Soderlund C., Spradon L., Stewart C.A., Sulston J.E., Swann R.M., Vandin M., Wall M., Wallis J.M., Whitley M.N., Willey D., Williams L., Williams S., Williamson H., Wilmer T.E., Wilming L., Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N., Minoshima S., Kawasaki K., Sakai T., Asakawa S., Kudoh J., Shintani A., Shibuya K., Yoshiaki Y., Aoki N., Mitsuyama S., Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T., Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I., Lewis J., Lewis S., Lin S., Loh P., Malaj E., Nguyen T., Pan H., Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L., Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z., Zhan M., Zhang G., Chlissos S., Murray J., Miller N., Mink P., Fulton R., Johnson D., Beninis G., Bentley D., Bradshaw H., Bourne S., Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J., Hinds K., Kemp K., Lattreille P., Layman D., Ozersky P., Rohlfing T., Scheet P., Walker C., Wansley A., Wohlmann P., Pepin K., Nelson J., Korff T., Bedell J.A., Hillier L., Mardi E.B., Waterston R., Neilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P., Wilkinson P., Bodeiteich A., Hartman K., Hu X., RA Khan A.S., Lane L., Tilahun Y., Wright H., RT "The DNA sequence of human chromosome 22.", RL Nature 402:489-495(1999). [2]

RN [2]

RP SEQUENCE OF 1-1337 FROM N.A.

RX MEDLINE=2003925; PubMed=1912569;

RA Tothaker L.E., Gonzalez D.A., Tung N., Lemons R.S., le Beau M.M., Arnout M.A., Clayton L.K., Tenen D.G.,

RT "Cellular myosin heavy chain in human leukocytes: isolation of 5,"

RT clones, characterization of the protein, chromosomal localization, and upregulation during myeloid differentiation.";

RT Blood 78:1826-1833(1991). [3]

RN [3]

RP SEQUENCE OF 1-715 FROM N.A.

RX MEDLINE=91316803; PubMed=1860190;

RA Simons M., Wang M., McBride O.W., Kawamoto S., Yamakawa K., RA Gdula D., Adelstein R.S., Weir L., RT Human nonmuscle myosin heavy chains are encoded by two genes located on different chromosomes.";

RL Circ. Res. 69:530-539(1991). [4]

RN SEQUENCE OF 714-1960 FROM N.A.

RX MEDLINE=9013959; PubMed=1957836;

RA Saez C.G., Myers J.C., Shows T.C., Lehnwand L.A., "Human nonmuscle myosin heavy chain mRNA: generation of diversity through alternative polyadenylation.";

RT Proc. Natl. Acad. Sci. U.S.A. 87:1164-1168(1990). [5]

RN VARIANT DFNA17 HIS-705.

RX MEDLINE=20488656; PubMed=11023810;

RA Lalwani A.K., Goldstein J.A., Kelley M.J., Luxford W., Castelein C.M., Mhatte A.N., "Human nonsyndromic hereditary deafness DFNA17 is due to a mutation in nonmuscle myosin MYH9";

RT Am. J. Hum. Genet. 67:1121-1128(2000). [6]





FT VARSPLIC 2441 2704 MISSING (IN ISOFORM 4).  
 FT CONFLICT 1998 1998 G -> R (IN REF. 5).  
 SQ SEQUENCE 2704 AA; 313084 MW; A7219E687A634A77 CRC64;

Query Match 7.0%; Score 166; DB 1; Length 2704;  
 Best Local Similarity 20.0%; Pred. No. 0.54; Mismatches 181; Indels 120; Gaps 19;  
 Matches 97; Conservative 88; Mismatches 181; Indels 120; Gaps 19;

QY 33 CLIQSFERAPSRSRCPQCRIQVKRTIINKLFLDQAQEEVNLDREFLKLNDLNVR----- 88  
 Db 1385 CRENALPVCPITQATSERAVT-----LOOBHDKORRAEKKQVDELTAAANRK 1432

QY 89 -----Q1SQDKKERRDSQVIDTRDTIEERNVVSIQQALGKAEMLCSTLKKQ 138  
 Db 1433 AEDMRELYTVELNQLAQLEKTSSSEKARLKLKDDETNTLRLCKLERKDOAEKGVSQ 1492

QY 139 MKYLEQQDET---KAQEEGGLRERMKTMQIEL-----LQSOLFEVEMIRD 1816  
 Db 1493 LRELGIGRQLNOTTGRKAEAMQEASDLK-KIRNYQOLELESNLHKGKLQR---EVDRITRA 1548

QY 187 MGIVGQSAVEQL-AVIVCSLKKEVYENLKEARKSGEVADKLRLDFSSRSRQLOTVYSEL 244  
 Db 1549 HAYAEKNTQHLSNSQHSRDEKLKLERLQICORESHRKEFER--SHEQOLNIKE 1605

QY 245 OAKKELKSAQKDIQSADKEIMSKKKLMLQETNLNPVASETV---DRLVIESPAVVE 300  
 Db 1606 NND-KIQRLNEEREKNSNCAEMKQKVLELTRONNETKLMMPQIASENIVLQHQ 1664

QY 301 --WNLKLRPSPFDIDINATEFVDTPPARPPSSQHGYYEKLICKLEHKSPIDVPKICK 358  
 Db 1665 RCFLALKILOADGFKDQL-----RSTNHE-----LHKQTKEEQDFORKI-- 1701

QY 359 GPKESQSLSGGSCAGE---PEELYGAFF-----IFVRVAILGOKQPRPRSSSC 408  
 Db 1702 -----KCLEDLAKSQNLAQSFQKCDQONITI--KKEVRLNLAELNA 1745

Db 409 SKDVVTGFGLGCRTKFIQPTDVMRPLPVPKTKVQRYFVKTPS-----LFO 460  
 Db 1746 SKERKRSEQKVQLQQAQVQELNNRL-----KKVQDELHLKLTIEQMTHRMVLFQ 1796

QY 461 AKLDTF 466

Db 1797 EESGKF 1802

RESULT 26

USOL\_YEAST STANDARD; PRT; 1790 AA.

ID P23386; 01-MAY-1992 (Rel. 22, Created)  
 DT 16-OCT-2001 (Rel. 40, last annotation update)  
 DE Intracellular protein transport protein in USOL

GN USOL OR INT1 OR VIM058W.

OS Saccharomyces cerevisiae (Baker's Yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

NCBI\_TaxID=4932;

RN [1] SEQUENCE FROM N.A.

RP STRIN=p210-1A;  
 MEDLINE=91183402; PubMed=2010462;

RA Nakajima H., Hirata A., Ogawa Y., Yonehara T., Yoda K.,  
 Yamasaki M.; "A cytoskeleton-related gene, usol, is required for intracellular protein transport in *Saccharomyces cerevisiae*.", J. Cell Biol. 113:245-260(1991).

RA Hostetter M.K., Herman D.J., Bendel C.M., McClellan M., Tao N., Kenardick K.E.; Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.

RN [3] SEQUENCE OF 1-8 FROM N.A..  
 RP Ba J.Y., Symington L.S.; Submitted (May-1996) to the EMBL/GenBank/DBJ databases.

RN [4] FUNCTION: REQUIRED FOR PROTEIN TRANSPORT FROM THE ER TO THE GOLGI COMPLEX.

RN [5] SUBCELLULAR LOCATION: CYTOPLASMIC. ASSOCIATED WITH INTRACELLULAR MEMBRANES. PROBABLY PRESENT ON VESICLES OPERATIONAL BETWEEN THE ER AND THE GOLGI COMPLEX.

RN [6] DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, COMPOSED OF AN HEPTEAPEPTIDE REPEAT PATTERN CHARACTERISTIC OF ALPHA-HELICAL COILED COILS. MAY FORM FILAMENTOUS STRUCTURES IN THE CELL.

RN [7] SIMILARITY: BELONGS TO THE VDP/USOL/YBL047C FAMILY.

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RN [9] EMBL; X54378; CAA3823; 1; -;

DR EMBL; U53666; AAB66659; 1; -;

DR PIR; A38455; A38455.

DR SGD; S000216; US01.

DR InterPro; IPR02017; Spectrin.

KW Protein transport; Golgi stack; cytoskeleton; coiled coil.

FT DOMAIN 1 724 GLOBULAR HEAD.

FT DOMAIN 725 1790 COILED COIL (POTENTIAL).

FT DOMAIN 465 487 CHARGED (HYPER-HYDROPHILIC).

FT DOMAIN 991 1790 DISPENSABLE FOR THE PROTEIN FUNCTION.

FT DOMAIN 1172 1786 ASP/GLU-RICH (ACIDIC).

FT CONFLICT 847 847 G -> E (IN REF. 2).

FT CONFLICT 924 924 E -> K (IN REF. 2).

FT CONFLICT 1253 1253 V -> I (IN REF. 2).

FT CONFLICT 1319 1319 I -> V (IN REF. 2).

FT CONFLICT 1461 1461 N -> S (IN REF. 2).

FT CONFLICT 1581 1581 G -> S (IN REF. 2).

FT CONFLICT 1600 1600 I -> V (IN REF. 2).

FT CONFLICT 1661 1661 R -> S (IN REF. 2).

FT CONFLICT 1772 1772 D -> DEEDEE (IN REF. 2).

FT SEQUENCE 1790 AA; 206424 MW; 6CE2B216E9FFD4818 CRC64;

Query Match 6.9%; Score 165.5; DB 1; Length 1790;  
 Best Local Similarity 20.9%; Pred. No. 0.36; Mismatches 129; Indels 91; Gaps 13;  
 Matches 78; Conservative 75; Mismatches 129; Indels 91; Gaps 13;

QY 55 KRTLINKLEFLDQA---BEENVLDREFL-----NLDNVRAQLSQKKEKRSQV 102  
 Db 1368 ERKLINESESTITQEYSRINTEDDELLRFLQNLNEKAKKEIDWTRSEL-EKYLSND--- 1423

QY 103 IIDTLRDTIEERNVVSIQQAL-----GKAEMLCSTLKKQMKVIEQQDETQKQAE 154  
 Db 1424 -----ELIEEKQNTIKSQDELSYKVKTRNDKEULSIERLNKRDLESQVRAQE 1477

QY 155 EAGRURSKRKTMRQDIELLIQSLQPEVEENIRDKGVGOSAVE---Q1AVYCSLKEVEN 210  
 Db 1478 SKAVVEGGLKLEBESEKKEAKELSKEMMKL---ESTIESNETELKSSMETIRKSDEK 1534

QY 211 LKEARKASSEVADKL-----KDLFSSRSKLOTVY--SELQDAKLEKSA 253  
 Db 1535 LEQSKSAEEDIKMLQHEQEDSLRINSESEKDEELKLKRRIFAKSSSELETVQELINA 1594

QY 254 QDKLQASADEKIMSKKLMLQETNLNPVASETVDRLVIESPAVVE-----LKLRR 307  
 Db 1595 QEKRINAINENTVLSKL-----EDIEREKLKQAEIKSNQEEKEULSRL 1640

QY 308 PSFRDIDINATEFVDTPPARPPSSQHGYEK-----LCLERKSHSP-----Q 350











[3]  
 RP  
 RA  
 RT  
 RC  
 STRAIN:968 HB0;  
 Ding D.;  
 "Generation and analysis of GFP-gene fusion library of fission  
 yeast;"  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.  
 RT -!- FUNCTION: AFTER THE ONSET OF MITOSIS, AT MID- TO LATE ANAPHASE,  
 CC CO-LOCALIZES WITH THE MEDIAL ACTIN RING. MAY PLAY A ROLE IN  
 CC CYTOKINESIS.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC use by non profit institutions as long as its content is in no way  
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 CC or send an email to license@isb-sib.ch).  
 CC  
 DR EMBL; ALI3357; CAB6214.1;  
 DR EMBI; ALI0473; AAB65416.1; ALT\_INIT.  
 DR EMBI; ABB028012; BAA87316.1; -. .  
 KW Coiled coil.  
 FT DOMAIN 57 361 COILED COIL (POTENTIAL).  
 FT DOMAIN 443 463 COILED COIL (POTENTIAL).  
 FT DOMAIN 54 740 COILED COIL (POTENTIAL).  
 FT DOMAIN 804 1106 COILED COIL (POTENTIAL).  
 FT DOMAIN 1223 1427 COILED COIL (POTENTIAL).  
 FT DOMAIN 1497 1555 COILED COIL (POTENTIAL).  
 FT DOMAIN 1601 1664 COILED COIL (POTENTIAL).  
 SEQUENCE 1727 AA; 197858 MW; F820BF8PC132644 CRC64;  
 SQ

ID MYHA\_HUMAN STANDARD; PRT; 1976 AA.  
 AC P55580;  
 DT 01-FEB-1996 (Rel. 29, Created)  
 DT 01-JUN-2001 (Rel. 40, Last annotation update)  
 DE Myosin heavy chain, nonmuscle type B (Cellular myosin heavy chain,  
 DE type B) (Nonmuscle myosin heavy chain-B) (NMNHC-B).  
 GN MYH10.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 RN NCBI\_TaxID9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-96025507; PubMed-7499478;  
 RA Phillips C.L., Yamakawa K., Adelstein R.S.;  
 RT "Cloning of the cDNA encoding human nonmuscle myosin heavy chain-B and  
 analysis of human tissues with isoform-specific antibodies.";  
 RL J. Muscle Res. Cell Motil. 16:379-389(1995).  
 RN [2]  
 RP SEQUENCE OF 63-722 FROM N.A.  
 RX MEDLINE-91131603; PubMed-1860190;  
 RA Simons M., Wang M., McBride O.W., Kawamoto S., Yamakawa K.,  
 RA Gaula D., Adelstein R.S., Weir L.;  
 RT "Human nonmuscle myosin heavy chains are encoded by two genes located  
 on different chromosomes";  
 RL Circ. Res. 69:530-539(1991).  
 CC -!- FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE IN CYTOKINESIS,  
 CC CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION AND  
 CC CAPPING.  
 CC -!- SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY  
 CC CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2



**KW** structural protein; Alternative splicing.

**FT** DOMAIN 1 1056 GLOBULAR 1.

**FT** DOMAIN 1057 1945 CENTRAL FIBROUS ROD DOMAIN.

**FT** DOMAIN 1946 2871 GLOBULAR 2.

**FT** REPEAT 347 447 SPECTRIN 1.

**FT** REPEAT 858 952 SPECTRIN 2.

**FT** DOMAIN 1018 1945 COTLED COIL (POTENTIAL).

**FT** REPEAT 2009 2045 PLECTIN 1.

**FT** REPEAT 2045 2083 PLECTIN 2.

**FT** REPEAT 2084 2121 PLECTIN 3.

**FT** REPEAT 2122 2159 PLECTIN 4.

**FT** REPEAT 2163 2197 PLECTIN 5.

**FT** REPEAT 2198 2233 PLECTIN 6.

**FT** REPEAT 2251 2288 PLECTIN 7.

**FT** REPEAT 2289 2326 PLECTIN 8.

**FT** REPEAT 2327 2364 PLECTIN 9.

**FT** REPEAT 2365 2402 PLECTIN 10.

**FT** REPEAT 2406 2440 PLECTIN 11.

**FT** REPEAT 2456 2493 PLECTIN 12.

**FT** REPEAT 2507 2544 PLECTIN 13.

**FT** REPEAT 2610 2647 PLECTIN 14.

**FT** REPEAT 2648 2685 PLECTIN 15.

**FT** REPEAT 2764 2761 PLECTIN 16.

**FT** REPEAT 2762 2799 PLECTIN 17.

**FT** DOMAIN 2824 2847 6 X 4 AA TANDEM REPEATS OF G-S-R-[SR] INTERACTS WITH PLAKOPHILIN 1 AND JUNCTION PLAKOGLOBIN.

**FT** MOD\_RES 2849 2849 PHOSPHORYLATION (BY CARK) (POTENTIAL).

**FT** VARSPLIC 1195 1794 MISSING (IN ISOFORM DP1).

**FT** VARSPLIC 905 905 R -> A (IN REF. 2).

**FT** CONFLICT 1120 1120 D -> R (IN REF. 3).

**FT** CONFLICT 2687 2688 SV -> RL (IN REF. 2).

**FT** SEQUENCE 2871 AA; 331771 MW; 5639B5B7CD4690B7 CRC64;

**Query Match** 6.9%; Score 163.5; DB 1; length 2871; Best Local Similarity 20.3%; Pred. No. 0.77; Mismatches 156; Indels 125; Gaps 22; Matches 96; Conservative 96; Mismatches 156; Indels 125; Gaps 22;

**QY** 15 DHSDVDAIHCGTFHQCLQSFETAPSRSRCPQCRIQVKTITINKLEFDLAQEEENVL 74

**Db** 1187 EYNEELAKVNRHNEEMLSNLNRKYET-----EINIKTYT-----KEISMQED-- 1230

**QY** 75 DREFLKNELDNVRQLSQDKKERRQDQVID--TLRDTLEERNATVVSLOQALGKAEMLC 132

**Db** 1231 DSKNLRNQD---RLSRNDRDIDELTVRLNDSSILQATEQRERAEVNLQKRCAGSEIMQ 1286

**QY** 133 ST--LKKMVKYIQQDDET---KQAQEAGR--LRSKMTMQEIQELIQ-----S 175

**Db** 1287 KKHTETELKQWQQRSEDNARKHQSLLEAKTIQDNKNEIERKAFQEEAKRRWEYEN 1346

**QY** 176 QLEEV----EEM-----RDMGVQASAVDGLAVY---CVSLKKEYENIKEARASG 219

**Db** 1347 ELSKVNNDIEEFTISLKNQFETETINIKTTIHLTMKEEDTSYQRQIDNTRENSL 1406..

**QY** 220 EVNDKLRLDFSSRSKLOTVYSELQAK-----LELKA-----Q 254

**Db** 1407 EETKRLKMLPTQTENLRVEEDIOQQRATGSVSQRKQLEVLRQVTQMRTEESVYK 1466

**QY** 255 KDIQSADKEIMSKKLTMLQETLNLPVVASETWDYLQLESAPVNEUNKLRRPSFRDDI 314

**Db** 1467 OSDDAAKTIQDNKELTRKQID---KEENDRCKLE---DENARLQRVOY--- 1512

**QY** 315 DMATDFTTPPARPSQSHQGY-----YEKICLEKSHSPIDOVPKICKSPRKESQLS 367

**Db** 1513 DIAKANSAATETINKLKVQEETITRLRDYERSQSERIVKD QDITR--FQNSLIKEQLQ 1569

**QY** 368 LGGSCAGEPDEFELVGAFPIFVNAILGOKQPRPSSECSKDVWRFGDL 420

**Db** 1570 -----KORVEEL-----NRLKRTASBDCKRKLEBELEGW 1601

**MYH7\_HUMAN**

**ID** MYH7\_HUMAN STANDARD; PRT; 1935 AA.

**AC** P12883; 01/04/04; 016579;

**DT** 01-OCT-1989 (Rel. 12, Created)

**DT** 01-JUN-1994 (Rel. 29, Last sequence update)

**DT** 16-OCT-2001 (Rel. 40, Last annotation update)

**DE** Myosin heavy chain, cardiac muscle beta isoform (MYHC-beta).

**GN** MYH7 OR MYHB.

**OS** Homo sapiens (Human).

**OC** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

**OC** Mammalia; Euarchontoglires; Eutheria; Primates; Catarrhini; Hominidae; Homo.

**OX** NCBI\_TaxId:9606;

**RN** [1]

**RP** SEQUENCE FROM N.A.

**RX** MEDLINE:91055634; PubMed=2249844;

**RA** Jaenicke T., Diedrich K.W., Haas W., Schleich J., Lichter P.,

**RA** Pfordt M., Bach A., Vosberg H.P.

**RT** "The complete sequence of the human beta-myosin heavy chain gene and a comparative analysis of its product.";

**RL** Genomics 8:194-206(1990).

**RP** SEQUENCE FROM N.A.

**RX** MEDLINE:90301496; PubMed=23262820;

**RA** Liew C.-C., Sole M.J., Yamauchi-Takihara K., Kellam B.,

**RA** Anderson D.H., Lin L., Liew J.;

**RT** Complete sequence and organization of the human cardiac beta-myosin heavy chain gene.;

**RT** Nucleic Acids Res. 18:3647-3651(1990).

**RN** [3]

**RP** SEQUENCE OF 1-115 FROM N.A.

**RX** MEDLINE=89264452; PubMed=2726733;

**RA** Yamauchi-Takihara K., Sole M.J., Liew J., Ing D., Liew C.-C.;

**RT** Characterization of human cardiac myosin heavy chain genes.;

**RL** Proc. Natl. Acad. Sci. U.S.A. 86:3504-3508(1989).

**RN** [4]

**RP** ERATUM.

**RA** Yamauchi-Takihara K., Sole M.J., Liew J., Ing D., Liew C.-C.;

**RL** Proc. Natl. Acad. Sci. U.S.A. 86:7416-7417(1989).

**RN** [5]

**RP** SEQUENCE OF 1310-1935 FROM N.A.

**RX** MEDLINE:86116778; PubMed=2421254;

**RA** Saez L., Leinwand L.A.:

**RT** Characterization of diverse forms of myosin heavy chain expressed in adult human skeletal muscle.;

**RT** Nucleic Acids Res. 14:2951-2969(1986).

**RN** [6]

**RP** REVISIONS.

**RA** Leinwand L.A.:

**RL** Submitted (MAR-1988) to the EMBL/GenBank/DDBJ databases.

**RN** [7]

**RP** SEQUENCE OF 1410-1935 FROM N.A.

**RX** MEDLINE:88229163; PubMed=2969919;

**RA** Kurabayashi M., Tsuchimochi H., Komuro I., Takaku F., Yazaki Y.;

**RA** "Molecular cloning and characterization of human cardiac alpha- and beta-form myosin heavy chain complementary DNA clones. Regulation of expression during development and pressure overload in human atrium";

**RT** J. Clin. Invest. 82:524-531(1988).

**RN** [8]

**RP** SEQUENCE OF 785-1935 FROM N.A.

**RC** TISSUE=Skeletal muscle;

**RT** MEDLINE:9023562; PubMed=1691980;

**RA** Bober E., Buchberger-Seidl A., Braun T., Singh S., Goedde H.W.,

**RA** Arnold H.H.;

**RT** "Identification of three developmentally controlled isoforms of human myosin heavy chains.;"

**RL** Eur. J. Biochem. 189:55-65(1990).

**RN** [9]

**RP** SEQUENCE OF 1393-1935 FROM N.A.

**RX** MEDLINE:87193738; PubMed=3032769;

**RA** Jandreski M.A., Liew C.-C.;

**RT** "Construction of a human ventricular cDNA library and characterization of a beta myosin heavy chain cDNA clone.;"

- RL Hum. Genet. 76:47-53(1987).  
 RN [10] RX  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE=96039076; PubMed=8533830;  
 RA Arai S., Matsuo K., Hirayama H., Tamura M., Ozawa T.,  
 RA Kimura M., Imamura S.-I., Kawana M., Takeo A.,  
 RA Hosoda S., Momma K.;  
 RT "Missense mutation of the beta-cardiac myosin heavy-chain gene in  
 RT hypertrophic cardiomyopathy";  
 RL Am. J. Med. Genet. 58:267-276(1995).  
 RN [11] RX  
 RP VARIANTS CMH1 GLU-256 AND ARG-741.  
 RX MEDLINE=93248216; PubMed=8433915;  
 RA Fananapazir L., Dalakas M.C., Cyran F., Cohn G., Epstein N.D.;  
 RT "Missense mutations in the beta-myosin heavy-chain gene cause central  
 core disease in hypertrophic cardiomyopathy";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:3993-3997(1993).  
 RN [12] RX  
 RP VARIANT CMH1 GLN-403.  
 RX MEDLINE=9036731; PubMed=195517;  
 RA Geisterer-Lowrance A.A.T., Kass S., Tanigawa G., Vosberg H.-P.,  
 RA McKenna W., Seidman C.E., Seidman J.G.;  
 RT "A molecular basis for familial hypertrophic cardiomyopathy: a beta  
 cardiac myosin heavy chain gene missense mutation";  
 RL Cell 62:999-1006(1990).  
 RN [13] RX  
 RP VARIANTS CMH1 GLN-249; GLN-403; CYS-453 AND MET-606.  
 RX MEDLINE=92204193; PubMed=1529212;  
 RA Watkins H., Rosenzweig A., Hwang D.S., Levi T., McKenna W.,  
 RA Seidman C.E., Seidman J.G.;  
 RT "Characteristics and prognostic implications of myosin missense  
 mutations in familial hypertrophic cardiomyopathy";  
 RL New Engl. J. Med. 326:1108-1114(1992).  
 RN [14] RX  
 RP VARIANTS CMH1 GLN-403; CYS-453; ARG-584 AND MET-606.  
 RX MEDLINE=9407063; PubMed=8250038;  
 RA Watkins H., Thierfelder L., Anan R., Jarcho J., Matsumori A.,  
 RA McKenna W., Seidman C.E., Seidman J.G.;  
 RT "Independent origin of identical beta cardiac myosin heavy-chain  
 RT mutations in hypertrophic cardiomyopathy";  
 RL Am. J. Hum. Genet. 53:1180-1185(1993).  
 RN [15] RX  
 RP VARIANTS CMH1 GLN-403 AND VAL-908.  
 RX MEDLINE=92168730; PubMed=1638703;  
 RA Epstein N.D., Cyran F., Fananapazir L.;  
 RT "Differences in clinical expression of hypertrophic cardiomyopathy  
 associated with two distinct mutations in the beta-myosin heavy chain  
 gene. A 908Leu-->Val mutation and a 403Arg-->Gln mutation";  
 RL Circulation 86:345-352(1992).  
 RN [16] RX  
 RP VARIANTS CMH1 LEU-403 AND TRP-403.  
 RX MEDLINE=94075629; PubMed=8224035;  
 RA Dausse E., Komajda M., Fettler L., Dubourg O., Dufour C., Carrier L.,  
 RA Wisniewsky C., Bercovicci J., Hengstenberg C., Al-Mahdawi S.,  
 RT "Familial hypertrophic cardiomyopathy. Microsatellite haplotyping and  
 RT identification of a hot spot for mutations in the beta-myosin heavy  
 RT chain gene";  
 RL Clin. Invest. 92:2807-2813(1993).  
 RN [17] RX  
 RP VARIANT CMH1 TRP-403.  
 RX MEDLINE=94093568; PubMed=8248932;  
 RA Moldman J.C., Brink P.A., Corfield V.A.;  
 RT "Identification of a new missense mutation at Arg403, a CPG mutation  
 hotspot, in exon 13 of the beta-myosin heavy chain gene in  
 hypertrophic cardiomyopathy";  
 RL Hum. Mol. Genet. 2:1731-1734(1993).  
 RN [18] RX  
 RP VARIANT CMH1 ASN-615.  
 RX MEDLINE=9303668; PubMed=1417858;  
 RA Nishi H., Kimura A., Harada H., Toshima H., Sasaki T.;  
 RT "Novel missense mutation in cardiac beta myosin heavy chain gene  
 found in a Japanese patient with hypertrophic cardiomyopathy";  
 RL Biochem. Biophys. Res. Commun. 188:379-387(1992).  
 RN [19] RX  
 RP VARIANT CMH1 GLY-778.  
 RX MEDLINE=9334938; PubMed=8343162;  
 RA Harada H., Kimura A., Nishi H., Sasazuki T., Toshima H.;  
 RT "A missense mutation of cardiac beta-myosin heavy chain gene linked  
 families";  
 RT to familial hypertrophic cardiomyopathy in affected Japanese  
 families";  
 RT Biochem. Biophys. Res. Commun. 194:791-798(1993).  
 RN [20] RX  
 RP VARIANT CMH1 VAL-908.  
 RX MEDLINE=93168485; PubMed=8435239;  
 RA Al-Mahdawi S., Chamberlain S., Cleland J., Nihoyannopoulos P.,  
 RA Gilligan D., French J., Choudhury L., Williamson R., Oakley C.;  
 RT "Identification of a mutation in the beta cardiac myosin heavy chain  
 gene in a family with hypertrophic cardiomyopathy";  
 RL Br. Heart J. 69:136-141(1993).  
 RN [21] RX  
 RP VARIANT CMH1 TRP-719.  
 RX MEDLINE=95179132; PubMed=7874131;  
 RA Greve G., Bachinski L., Friedman D.L., Czernuzewicz G., Anan R.,  
 RA Townin J., Seidman C.E., Roberts R.;  
 RT "Isolation of a de novo mutant myocardial beta MHC protein in a  
 RT pedigree with hypertrophic cardiomyopathy";  
 RL Hum. Mol. Genet. 3:2073-2075(1994);  
 RN [22] RX  
 RP VARIANTS CMH1 CYS-513; ARG-716 AND TRP-719.  
 RX MEDLINE=94110336; PubMed=82202798;  
 RA Anan R., Greve G., Thierfelder L., Watkins H., McKenna W., Solomon S.,  
 RA Vecchio C., Shono H., Nakao S., Tanaka H., Mares A. Jr., Towbin J.A.,  
 RA Spirito P., Roberts R., Seidman J.G., Seidman C.E.;  
 RT "Prognostic implications of novel beta cardiac myosin heavy chain gene  
 mutations that cause familial hypertrophic cardiomyopathy";  
 RL J. Clin. Invest. 93:280-285(1994).  
 RN [23] RX  
 RP VARIANT CMH1 THR-797.  
 RX MEDLINE=96041759; PubMed=781410;  
 RA Moorman J.C., Brink P.A., Corfield V.A.;  
 RT "Identification of a novel Ala79Thr mutation in exon 21 of the beta-  
 RT myosin heavy chain gene in hypertrophic cardiomyopathy";  
 RL Hum. Mutat. 6:197-198(1995).  
 RN [24] RX  
 RP VARIANT CMH1 CYS-453.  
 RX MEDLINE=96205901; PubMed=8655135;  
 RA Ko Y.-L., Chen J.-J., Tang C.-K., Cheng J.-J., Lin S.-Y., Liou Y.-C.,  
 RA Kuan P., Wu C.-W., Lien W.-P., Liaw C.-C.;  
 RT "Malignant familial hypertrophic cardiomyopathy in a family with a  
 RT 53Arg-->Cys mutation in the beta-myosin heavy chain gene: a  
 RT coexistence of sudden death and end-stage heart failure";  
 RL Hum. Genet. 97:585-590(1996).  
 RN [25] RX  
 RP VARIANTS CMH1 THR-349 AND TRP-719.  
 RX MEDLINE=98204402; PubMed=9344842;  
 RA Jeschke B., Uhl K., Weist B., Schroder D., Meitinger T.,  
 RA Donalmann C., Vosberg H.-P.;  
 RA "A high risk phenotype of hypertrophic cardiomyopathy associated with  
 RT Query Match 6.8%; Score 163; DB 1; Length 1935;  
 Best Local Similarity 22.1%; Pred. No. 0.52; Gaps 9;  
 Matches 64; Conservative 62; Mismatches 107; Indels 56; Gaps 9;
- |    |  |      |
|----|--|------|
| Qy | 31. LOCLIQSFETAPSRTPCOPRCRQVGRKTFLINKLFFDLAQEEENVLDRF-----           | 78   |
| Db | 1143 LEEETSERLEEAAGGATSVOLEMKKREAEFFOKMRDL---EATLQHETAAALKRHADS      | 1199 |
| Qy | 79 --LKNEDNVRAQLSQDKERDSQVITDTURDLEBERRNATWLSQQLGKRAEMCSTL 135       |      |
| Db | 1200 VAEIGEQIDNLQVKQKLEKESEFKLEDDYTSNMQ-----IKAKANLEKMCRTL 1252      |      |
| Qy | 136 KKQKYLEQQDETQKQAEAGRLSKMT-----MEQTELLIQSQLP-----                 | 178  |
| Db | 1253 EDQMEHRSSKAERTQRSVNDLTSQRKLQTEGELSQDEREALI-SQJTRGKLTYTQ 1311    |      |
| Qy | 179 -----EVEEMIRDGMVGOSAVEOLAVYVCVSLJKKEYENLKEARKASGEVADKLRLKDLS 232 |      |

RESULT 37  
**MISS\_CHICK** STANDARD; PRT; 1938 AA.  
 ID MISS\_CHICK STANDARD; PRT; 1938 AA.  
 AC PI3538: 013228;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Myosin heavy chain, skeletal muscle, adult.  
 OS Gallus gallus (chicken).  
 EA Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.;  
 RC TISSUE=WHITE LEGHORN; TISSUE=Pectoralis muscle;  
 RA Chao T.H., Bandman E., Moore L.;  
 RT "Cloning, nucleotide sequence and characterization of a full-length cDNA encoding the myosin heavy chain from adult chicken pectoralis major muscle"; Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE OF 1-205  
 RC TISSUE=Pectoralis muscle;  
 RX MEDLINE=92041767; PubMed=1039027;  
 RA Hayashida M., Maita T., Matsuda G.;  
 RT "The primary structure of skeletal muscle myosin heavy chain: I. Sequence of the amino-terminal 23 kDa fragment.", J. Biochem. 110:54-59(1991).  
 RN [3]  
 SEQUENCE OF 206-636.  
 RC TISSUE=Pectoralis muscle;  
 RX MEDLINE=92041768; PubMed=1039028;  
 RA Komine Y., Maita T., Matsuda G.;  
 RT "The primary structure of skeletal muscle myosin heavy chain: II. Sequence of the 50 kDa fragment of subfragment-1.", J. Biochem. 110:60-67(1991).  
 RN [4]  
 SEQUENCE OF 637-837.  
 RC TISSUE=Pectoralis muscle;  
 RX MEDLINE=92041769; PubMed=1039029;  
 RA Maita T., Miyashita T., Matsuzono K., Tanioka Y., Matsuda G.;  
 RT "The primary structure of skeletal muscle myosin heavy chain: III. Sequence of the 22 kDa fragment and the alignment of the 23 kDa, 50 kDa, and 22 kDa fragments.", J. Biochem. 110:68-74(1991).  
 RN [5]  
 SEQUENCE OF 838-1938.  
 RC TISSUE=Pectoralis muscle;  
 RX MEDLINE=92041770; PubMed=1039030;  
 RA Maita T., Yajima E., Nagata S., Miyashita T., Nakayama S., Matsuda G.;  
 RT "The primary structure of skeletal muscle myosin heavy chain: IV. Sequence of the rod, and the complete 1,938-residue sequence of the heavy chain.", J. Biochem. 110:75-87(1991).  
 RN [6]  
 PRELIMINARY SEQUENCE OF 1-808.  
 RX MEDLINE=87093420; PubMed=347365;  
 RA Maita T., Hayashida M., Tanioka Y., Komine Y., Matsuda G.;  
 RT "The primary structure of the myosin head.", Proc. Natl. Acad. Sci. U.S.A. 84:415-420(1987).  
 RP SEQUENCE OF 842-1370.  
 RX MEDLINE=90121764; PubMed=26310940;  
 RA Watanabe B.;

RT "Complete amino-acid sequence of subfragment-2 in adult chicken skeletal muscle myosin.", Biol. Chem. Hoppe-Seyler 370:1027-1034(1989).  
 RN [8]  
 SEQUENCE OF 852-1108.  
 RX MEDLINE=893744803; PubMed=2775482;  
 RA Watanabe B.;  
 RT "Amino-acid sequence of the short subfragment-2 in adult chicken skeletal muscle myosin.", Biol. Chem. Hoppe-Seyler 370:549-558(1989).  
 RN [9]  
 SEQUENCE OF 1145-1270.  
 RX MEDLINE=89228549; PubMed=2713098;  
 RA Watanabe B.;  
 RT "Amino-acid sequence of the hinge region in chicken myosin subfragment-2.", Biol. Chem. Hoppe-Seyler 370:55-61(1989).  
 RN [10]  
 SEQUENCE OF 1857-1938 FROM N.A.  
 RX MEDLINE=87217964; PubMed=3034534;  
 RA Moriarity D.M., Barringer K.J., Dodgson J.B., Richter H.E., Young R.B.;  
 RT "Genomic clones encoding chicken myosin heavy-chain genes.", DNA 6:91-99(1987).  
 RN [11]  
 X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 1-843.  
 RX MEDLINE=93305624; PubMed=8316857;  
 RA Rayment I., Rypniewski W.R., Schmidt-Base K., Smith R., Tomchick D.R., Benning M.M., Winkelmann D.A., Wesenberg G., Holden H.M.;  
 RA "Three-dimensional structure of myosin subfragment-1: a molecular motor.", Science 261:50-58(1993).  
 CC -!- FUNCTION: MUSCLE CONTRACTION. MYOSIN IS A PROTEIN THAT BINDS TO F-ACTIN AND HAS ATPASE ACTIVITY THAT IS ACTIVATED BY F-ACTIN.  
 CC -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (HIC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).  
 CC -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.  
 CC -!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 26-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.  
 CC -!- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.  
 CC -!- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LM) AND 1 HEAVY MEROMYOSIN (HM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).  
 CC -!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.  
 CC -!- SIMILARITY: CONTAINS 1 IQ DOMAIN.

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CC EMBL; U87231; AAB47551;  
 DR DR EMBL; M16557; AAA48970\_1; -.  
 DR PIR; PX0050; PX0051.  
 DR PIR; A26821; A26821.  
 DR PIR; S02082; S02082.  
 DR PIR; S04501; S04501.  
 DR PIR; S05515; S05515.  
 DR PIR; U87231; AAB47551.  
 DR PIR; PX0050; PX0051.  
 DR InterPro; IPRO04009; Myosin-N.  
 DR InterPro; IPRO02928; Myosin-tail.  
 DR InterPro; IPRO01609; myosin-head.  
 DR Pfam; PF00612; IQ; 2.  
 DR Pfam; PF0063; myosin\_head; 1.

[1] DR Pfam; PF02736; Myosin\_N; 1.  
DR Pfam; PF0176; Myosin\_tail; 1.  
DR PRO35; PD0035; myosin\_head; 1.  
DR SMART; SM0015; IQ; 1.  
DR PROSITE; PS50096; IQ; 1.  
DR Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;  
KW Calmodulin-binding; Multigene family; 3D-structure.  
FT INIT\_MET 0  
FT DOMAIN 1 782 MYOSIN HEAD-LIKE.  
FT DOMAIN 0 838 IQ.  
FT DOMAIN 1 840 HINGE.  
FT DOMAIN 1 841 1938 COILED COIL (POTENTIAL).  
FT DOMAIN 1 845 ATP (POTENTIAL).  
FT DOMAIN 1 849 NP\_BIND 185 ACTIN-BINDING.  
FT DOMAIN 1 853 657 679 MOD\_RES 1 1 ACETYLYATION.  
FT DOMAIN 1 857 759 773 MOD\_RES 35 35 METHYLATION (MONO-).  
FT DOMAIN 1 861 755 755 MOD\_RES 130 130 METHYLATION (TRI-).  
FT DOMAIN 1 865 697 697 MOD\_RES 130 130 METHYLATION (TRI-).  
FT DOMAIN 1 869 707 707 CONFLICT 907 907 ALKYLATION (SH-1).  
FT DOMAIN 1 873 707 707 CONFLICT 907 907 ALKYLATION (SH-2).  
FT DOMAIN 1 877 707 707 CONFLICT 907 907 C -> Q (IN REF. 7 AND 8).  
FT DOMAIN 1 881 707 707 CONFLICT 907 907 L -> F (IN REF. 1).  
FT DOMAIN 1 885 707 707 CONFLICT 907 907 E -> D (IN REF. 5).  
FT DOMAIN 1 889 707 707 CONFLICT 907 907 S -> A (IN REF. 5).  
FT DOMAIN 1 893 707 707 CONFLICT 907 907 HV -> OL (IN REF. 5).  
FT DOMAIN 1 897 707 707 CONFLICT 907 907 S -> A (IN REF. 5).  
FT DOMAIN 1 901 707 707 CONFLICT 907 907 I -> V (IN REF. 10).  
FT DOMAIN 1 905 707 707 CONFLICT 907 907 IHG -> FH (IN REF. 10).  
FT DOMAIN 1 909 707 707 CONFLICT 907 907 FETAL LIVER, SPLEEN, THYMUS AND ADULT THYMUS AND BONE MARROW.  
SQ 1929 1931 1938 AA; 223013 MW; EDD01CEA2681E1OF CRC64; LOWER LEVELS ARE FOUND IN HEART, TESTIS, KIDNEY, COLON AND LUNG.  
-----

Query Match Best Local Similarity 6.8%; Score 163; DB 1; Length 1938; Matches 65; Conservative 22.3%; Pred. No. 0..52; Mismatches 107; Indels 62; Gaps 9; QY 31 IQLCQSFETAPSRTCPQCRCVQKRITIINKLFFDLAQEEENVLDREF---- 78 Db 1145 LEEISERLLEAGGATAAQIEMKKREAFQMRRL--EETLQHEATAALRKHHADS 1201

QY 79 --LKNELDNYTAQOLSKDKRDSQVITDUTRDLEERRNATWVSQLQALGKRAEMICSTL 135 Db 1202 TAELEGQDINLQRVKORKEKESKLMEIDDLASNME----SVSKAKLEKMRTL 1254

QY 136 KKQMKLEQQDE-----TQQAEEBAGRL--RSKMKTWEQI 169 Db 1255 EDQLESEIKTKKEBQNORMINDNTQRARLQTGEYSQAAEKDALLSQLSRKGFTQQL 1314

QY 170 EILLOSQQLPEVEEMTRDMGVQGSASVAVOLAVVCGVSLKEYENLKEARKASGEVADKLKDL 229 Db 1315 EBLKR---HLEEEIKAKNALAHALOSARHDCCELLREQYEQQEAKGELQRALSANSFV 1370

QY 230 FSSRSKLOT---WVSELQAKLELSAQDQLQSASKEIMSKKLTMLQET 277 Db 1371 AQRWKTYETDAIORTBLEEAKKL--AQR-LQDAEHHVEANAKCSELEKT 1419

RESULT 38

KF4A\_HUMAN  
ID KF4A\_HUMAN STANDARD; PRT; 1232 AA.  
AC Q92339; Q9MMW3; Q9NNY6; Q9NY24;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Chromosome-associated kinesin KIF4A (Chromokinesin).  
DE Homo sapiens (Human).  
OS Homo sapiens OR KIF4.  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Osteichthyes; Tetrapoda; Amniota; Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.

NCBI\_TaxID:9606; OC 1  
OX

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CC DR EMBL: AF179308; AAD51855; 1..  
CC DR EMBL: AF071592; AAD05492; 2..  
CC DR EMBL: AJ2271784; CAB75427; 1..  
CC DR EMBL: AP277375; AAF86334; 1..  
CC DR HSSP; P1719; 3KAR.  
CC DR InterPro; IPRO01752; kinesin.  
CC DR Pfam; PF00225; kinesin\_1.  
CC DR PRINTS; PR0360; KINESINHEAVY.  
CC DR SMART; S00129; KISC\_1.  
CC DR PROSITE; PS0041; KINESIN\_MOTOR\_DOMAIN; 1.  
CC DR PROSITE; PS50067; KINESIN\_MOTOR\_DOMAIN; 1.  
CC DR Motor protein; Microtubules; ATP-bundles; ATP-binding; DNA-binding; KW Nuclear protein; Coiled coil.  
FT DOMAIN 1 349 KINESIN-MOTOR.  
FT DOMAIN 1 350 999 COILED COIL (BY SIMILARITY).  
FT DOMAIN 1000 1232 GLOBULAR.  
FT NP\_BIND 88 95 ATP (POTENTIAL).  
FT CONFLICT 223 223 R -> G (IN REF. 2).  
FT CONFLICT 231 231 S -> T (IN REF. 4).  
FT CONFLICT 286 286 V -> A (IN REF. 2).  
FT CONFLICT 422 422 L -> W (IN REF. 2).  
FT CONFLICT 564 564 L -> H (IN REF. 4).  
FT CONFLICT 564 564 L -> P (IN REF. 2).  
FT CONFLICT 600 600 K -> E (IN REF. 3).  
FT CONFLICT 668 668 R -> K (IN REF. 3 AND 4).  
FT CONFLICT 928 928 O -> P (IN REF. 1).  
FT CONFLICT 958 959 QL -> RL (IN REF. 3).  
FT CONFLICT 960 960 L -> Q (IN REF. 1).  
FT CONFLICT 996 997 LL -> S (IN REF. 4).  
FT CONFLICT 1003 1014 QKHPKDTLSP -> RTLPRTPEYLO (IN REF. 4).

[2] DR PRO35; PD0035; myosin\_head; 1.  
DR SMART; SM0015; IQ; 1.  
DR PROSITE; PS50096; IQ; 1.  
DR Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; ATP-binding; Methylation; Alkylation; Phosphorylation; Acetylation; Calmodulin-binding; Multigene family; 3D-structure.  
FT INIT\_MET 0  
FT DOMAIN 1 782 MYOSIN HEAD-LIKE.  
FT DOMAIN 0 838 IQ.  
FT DOMAIN 1 840 HINGE.  
FT DOMAIN 1 841 1938 COILED COIL (POTENTIAL).  
FT DOMAIN 1 845 ATP (POTENTIAL).  
FT DOMAIN 1 849 NP\_BIND 185 ACTIN-BINDING.  
FT DOMAIN 1 853 657 679 MOD\_RES 1 1 ACETYLYATION.  
FT DOMAIN 1 857 759 773 MOD\_RES 35 35 METHYLATION (MONO-).  
FT DOMAIN 1 861 755 755 MOD\_RES 130 130 METHYLATION (TRI-).  
FT DOMAIN 1 865 697 697 MOD\_RES 130 130 METHYLATION (TRI-).  
FT DOMAIN 1 869 707 707 CONFLICT 907 907 ALKYLATION (SH-1).  
FT DOMAIN 1 873 707 707 CONFLICT 907 907 ALKYLATION (SH-2).  
FT DOMAIN 1 877 707 707 CONFLICT 907 907 C -> Q (IN REF. 7 AND 8).  
FT DOMAIN 1 881 707 707 CONFLICT 907 907 L -> F (IN REF. 1).  
FT DOMAIN 1 885 707 707 CONFLICT 907 907 E -> D (IN REF. 5).  
FT DOMAIN 1 889 707 707 CONFLICT 907 907 S -> A (IN REF. 5).  
FT DOMAIN 1 893 707 707 CONFLICT 907 907 HV -> OL (IN REF. 5).  
FT DOMAIN 1 897 707 707 CONFLICT 907 907 S -> A (IN REF. 5).  
FT DOMAIN 1 901 707 707 CONFLICT 907 907 I -> V (IN REF. 10).  
FT DOMAIN 1 905 707 707 CONFLICT 907 907 IHG -> FH (IN REF. 10).  
FT DOMAIN 1 909 707 707 CONFLICT 907 907 FETAL LIVER, SPLEEN, THYMUS AND ADULT THYMUS AND BONE MARROW.  
SQ 1929 1931 1938 AA; 223013 MW; EDD01CEA2681E1OF CRC64;

SEQUENCE FROM N.A. [3]  
RP TISSUE=Lymphocytes;  
RC Villard L.;  
RA Submitted (AUG-1999) to the ENBLY/genBank/DDJB databases.  
RN [2]  
RA On S.J., Hahn H., Torrey T.A., Shin H., Choi W., Lee Y.M., Morse H.C. III, Kim W.;  
RT "Identification of the human homologue of mouse KIF4, a kinesin superfamily motor protein";  
RL Biochim. Biophys. Acta 1493:219-224 (2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Retinoblastoma;  
RA Rentsch A., Neumann T., Rommerskirch W.;  
RL Submitted (FEB-2000) to the EMBL/GenBank/DDJB databases.  
RN [4]  
RP SEQUENCE OF 128-1232 FROM N.A.  
RC TISSUE=Retinoblastoma;  
RA MEDLINE=97311419; Pubmed=9168136;  
RL "Increased chromokinesin immunoreactivity in retinoblastoma cells"; Gene 189:263-273 (1997).  
CC -- FUNCTION: REQUIRED FOR MITOTIC CHROMOSOMAL POSITIONING AND BIPOAR SPINDLE STABILIZATION (BY SIMILARITY).  
CC -- SUBCELLULAR LOCATION: NUCLEAR, ASSOCIATED WITH MITOTIC CHROMOSOMES (BY SIMILARITY).  
CC -- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEMATOPOIETIC TISSUES, FETAL LIVER, SPLEEN, THYMUS AND ADULT THYMUS AND BONE MARROW.  
CC -- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.  
CC -- CHROMOKINESIN SUBFAMILY.

SEQUENCE FROM N.A. [1]  
RP TISSUE=Lymphocytes;  
RC Villard L.;  
RA Submitted (AUG-1999) to the ENBLY/genBank/DDJB databases.  
RN [2]  
RA On S.J., Hahn H., Torrey T.A., Shin H., Choi W., Lee Y.M., Morse H.C. III, Kim W.;  
RT "Identification of the human homologue of mouse KIF4, a kinesin superfamily motor protein";  
RL Biochim. Biophys. Acta 1493:219-224 (2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Retinoblastoma;  
RA Rentsch A., Neumann T., Rommerskirch W.;  
RL Submitted (FEB-2000) to the EMBL/GenBank/DDJB databases.  
RN [4]  
RP SEQUENCE OF 128-1232 FROM N.A.  
RC TISSUE=Retinoblastoma;  
RA MEDLINE=97311419; Pubmed=9168136;  
RL "Increased chromokinesin immunoreactivity in retinoblastoma cells"; Gene 189:263-273 (1997).  
CC -- FUNCTION: REQUIRED FOR MITOTIC CHROMOSOMAL POSITIONING AND BIPOAR SPINDLE STABILIZATION (BY SIMILARITY).  
CC -- SUBCELLULAR LOCATION: NUCLEAR, ASSOCIATED WITH MITOTIC CHROMOSOMES (BY SIMILARITY).  
CC -- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEMATOPOIETIC TISSUES, FETAL LIVER, SPLEEN, THYMUS AND ADULT THYMUS AND BONE MARROW.  
CC -- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.



Matches	Conservative	Mismatches	84;	Indels	49;	Gaps	9;
QY	51	IQVGKRTIINKLFFLAQEEVNVLREFKLNL-DNVR--AOLSOKDEKKRSQVIIPT	106				
Db	1045	VEAKR---KVEQDLKSTOENVEDLERYKRELEENVRKEAEISLNSKLEDEONLVSQ	1100				
QY	107	LRTDLTEERNATVWSLQQALGKAMECSTLKKQMYLQQDDETKQAEEBAGRLSKMKM	166				
Db	1101	LQRKIKELQARIEELEELLEAERNAKARVQKARBLNEELBEGG----ATS	1155				
QY	167	EQEELLQSQLEPEEMIRDMVGVSQAVEOLAVICVSLKEYENIKEARKASGEVADLR	226				
Db	1156	AQIELNKRE-AELKIRDL--EASLOHEAQISALRKHQD-----AANEMADQV-	1204				
QY	227	KDLFSSRSKLOTVYSELDDQAKLKSQAKQLOSA-----DKEIMSLK	268				
Db	1205	--DOLQKVSKLEKDKDKLREMDDLESQMTNPKNNKGSEKVKMQFESQMSDLN	1257				
QY	269	KKLTMQETIN	279				
Db	1258	ARLEDSORSIN	1268				
<b>RESULT 40</b>							
<b>AKA9_HUMAN</b>							
ID	HUMAN	STANDARD;	PRT:	3911 AA.			
AC	09U0Q4; Q99QH3; 09Y6Y2; 014869; 043355; 094895; Q9Y6B8;						
DT	16-OCT-2001 (rel. 40, Created)						
DT	16-OCT-2001 (rel. 40, Last sequence update)						
DT	16-OCT-2001 (rel. 40, Last annotation update)						
DE	A-kinase anchor protein 9 (Protein kinase A anchoring protein 9)						
DE	(PRKA9) (A-kinase anchor protein 450 kDa) (AKAP 450) (A-kinase anchor protein 350 kDa) (AKAP 350) (AKAP 120 like protein)						
DE	(Hyperion protein) (Yotiao protein) (Centrosome- and golgi-localized PKN-associated protein) (CG-NAP)						
GN	AKAP9 OR AKAP450 OR KIAA0803.						
OS	Homo sapiens (Human);						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
OX	NCBI_TaxID=9606;						
RN	[1]						
RP	SEQUENCE FROM N.A. (ISOFORM 4).						
RC	TISSUE=Brain;						
RX	Medline=98151389; Pubmed=9482789;						
RA	Lin J.W., Wyszynski M., Madhavan R., Sealock R., Kim J.U., Sheng M.; "Yotiao," a novel protein of neuromuscular junction and brain that interacts with specific splice variants of NMDA receptor subunit NR1.";						
RL	J. Neurosci. 18:2017-2027(1998).						
RN	[2]						
RP	SEQUENCE FROM N.A. (ISOFORM 2), AND VARIANT GLN-1347 INS.						
RX	Medline=99219864; Pubmed=10202149;						
RA	Witzczak O., Shaalberg B.S., Keryer G., Bornens M., Tasken K., Jahnsen T., Oerstavik S.,						
RT	"Cloning and characterization of a cDNA encoding an A-kinase anchoring protein located in the centrosome, AKAP450.";						
RL	EMBO J. 18:1858-1868(1999).						
RN	[3]						
RP	SEQUENCE FROM N.A. (ISOFORM 3).						
RC	TISSUE=Brain;						
RX	Medline=9928734; Pubmed=10358086;						
RA	Takahashi M., Shibata H., Shimakawa M., Miyamoto M., Mukai H., Ono Y.; "Characterization of a novel giant scaffolding protein, CG-NAP, that anchors multiple signaling enzymes to centrosome and the golgi apparatus"; J. Biol. Chem. 274:17267-17274(1999).						
RL	J. Biol. Chem. 274:17267-17274(1999).						
RN	[4]						
RP	SEQUENCE FROM N.A. (ISOFORM 1).						
RA	Kemmer W.A., Deiss S., Schwarz U.; "Cloning of Hyperion.";						
RT	Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.						
RN	[5]						
RP	SEQUENCE OF 323-3911 FROM N.A. (ISOFORM 2).						
<b>TISSUE=Gastric parietal cell;</b>							
RC	Medline=9911554; Pubmed=9915845;						
RX	Schmidt P.H., Dransfield D.T., Claudio J.O., Hawley R.G., Trotter K.W., Milgram S.L., Goldenring J.R.; "AKAP350, a multiply spliced protein kinase A-anchoring protein associated with centrosomes"; J. Biol. Chem. 274:3055-3066(1999).						
RA	[6]						
RP	SEQUENCE OF 1802-3876 FROM N.A. (ISOFORM 5).						
RC	TISSUE=Lymphoblast;						
RA	Hinds K., Sutterer C., Becker M., Hawkins M.; "AKAP350: A multiply spliced family of proteins with centrosomal association." Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.						
RT	[7]						
RL	SEQUENCE OF 2157-3911 FROM N.A. (ISOFORM 6).						
RC	Milram S.L., Goldenring J.R., Schmidt P.H.; "AKAP350: A multiply spliced family of proteins with centrosomal association." Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.						
RA	[8]						
RP	SEQUENCE OF 2212-3911 FROM N.A. (ISOFORM 2/3).						
RC	TISSUE=Brain;						
RA	Nagase T., Isikawa K.-I., Suyama M., Kikuno R., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro"; DNA Res. 5:277-286(1998).						
RL	[9]						
RP	SEQUENCE OF 17-1800 FROM N.A.						
RA	Wu X., Graves T., Bradshaw H.; "Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.						
RC	The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro"; DNA Res. 5:277-286(1998).						
CC	-!- FUNCTION: BINDS TO TYPE II REGULATORY SUBUNITS OF PROTEIN KINASE PHOSPHATASES ON CENTROSOME AND GOLGI APPARATUS WHERE PHYSIOLOGICAL EVENTS CAN BE REGULATED BY PHOSPHORYLATION STATE OF PROTEIN SUBSTRATES. ISOFORM 4/YOTIAO IS ASSOCIATED WITH THE N-METHYL-D-ASPARTATE RECEPTOR AND IS SPECIFICALLY FOUND IN THE NEUROMUSCULAR JUNCTION (NMJ) AS WELL AS IN NEURONAL SNAPPES EXPLAINING THAT ITS ROLE MAY BE TO ORGANIZE POSTSYNAPTIC SPECIALIZATIONS.						
CC	-!- SUBUNIT: INTERACTS WITH THE REGULATORY REGION OF PROTEIN KINASE N (PKN). PROTEIN PHOSPHATASE 2A (PP2A), PROTEIN PHOSPHATASE 1 (PP1) AND THE IMMATURE NON-PHOSPHORYLATED FORM OF PKC EPSILON.						
CC	-!- SUBCELLULAR LOCATION: CENTROSOMAL IN MANY CELL TYPES AND CYTOPLASMIC IN PARTIAL CELLS.						
CC	-!- ALTERNATIVE PRODUCTS: 6 ISOFORMS: 1 (SHOWN HERE), 2, 3/CG-NAP, 4/YOTIAO, 5 AND 6/AKAP350; ARE PRODUCED BY ALTERNATIVE SPlicing.						
CC	-!- TISSUE SPECIFICITY: WIDELY EXPRESSED. ISOFORM 4/YOTIAO IS HIGHLY EXPRESSED IN SKELETAL MUSCLE AND IN PANCREAS.						
CC	-!- DOMAIN: RIT BINDING SITE, PREDICTED TO FORM AN AMPHIPATHIC HELIX, COULD PARTICIPATE IN PROTEIN-PROTEIN INTERACTIONS WITH A COMPLEMENTARY SURFACE ON THE R-SUBUNIT DIMER.						
CC	-!- CAUTION: REF. 6 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO TWO FRAMESHIFTS IN POSITIONS 3782 AND 3811.						
CC	-!- CAUTION: REF. 9 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FOUR FRAMESHIFTS IN POSITIONS 29, 1653, 1699 AND 1735.						
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).						
CC	[10]						
DR	EMBL: AJ131693; CAB40713; -						
DR	DR: AB019691; BAB78718; -						
DR	EMBL: A010770; CAB09361; -						
DR	EMBL: AF026245; AAB86384; -						
DR	EMBL: AF083037; AAD22767; -						
DR	EMBL: AC004013; AAB96867; ALT_FRAME.						

DR EMBL: AR091711; ADD39719.1; -  
 DR EMBL: AR018346; BRA34523.1; -  
 DR EMBL: AAC00006; AAC60380.1; ALT\_FRAME.  
 DR MM: 604001; -  
 KW Coiled coil; Alternative splicing; Polymorphism.  
 FT DOMAIN 2554 2567 ALTERNATIVE SPlicing; PoLYMORPhism.  
 FT DOMAIN 164 914 PTK-RRI SUBUNIT BINDING DOMAIN.  
 FT DOMAIN 944 1022 COILED COIL (POTENTIAL).  
 FT DOMAIN 1100 1185 COILED COIL (POTENTIAL).  
 FT DOMAIN 1253 1280 COILED COIL (POTENTIAL).  
 FT DOMAIN 1336 1392 COILED COIL (POTENTIAL).  
 FT DOMAIN 1434 1459 COILED COIL (POTENTIAL).  
 FT DOMAIN 1585 1659 COILED COIL (POTENTIAL).  
 FT DOMAIN 1857 2455 COILED COIL (POTENTIAL).  
 FT DOMAIN 2544 2561 COILED COIL (POTENTIAL).  
 FT DOMAIN 2603 2776 COILED COIL (POTENTIAL).  
 FT DOMAIN 3065 3092 COILED COIL (POTENTIAL).  
 FT DOMAIN 3124 3470 COILED COIL (POTENTIAL).  
 FT DOMAIN 3587 3689 COILED COIL (POTENTIAL).  
 FT DOMAIN 3726 3730 POLY-LEU.  
 FT DOMAIN 203 1010 GLU-RICH.  
 FT DOMAIN 1846 2772 GLU-RICH.  
 FT VARSPLIC 17 28 MISSING (IN ISOFORM 2 AND ISOFORM 3).  
 FT VARSPLIC 1642 1642 QLOQELI -> LATRRD (IN ISOFORM 4).  
 FT VARSPLIC 1643 3911 MISSING (IN ISOFORM 4).  
 FT VARSPLIC 2175 2182 SADFOKVE -> O (IN ISOFORM 6).  
 FT VARSPLIC 2175 2183 VFGTNYMCSTLC -> GSPIEALHSAYQTRBICSS  
 FT VARSPLIC 2895 2948 (IN ISOFORM 2, ISOFORM 3 AND ISOFORM 6).  
 FT VARSPLIC 3901 3911 MISSING (IN ISOFORM 5).  
 FT VARIANT 1347 1347 SLG (IN ISOFORM 6).  
 FT CONFLICT 76 76 /FTid=VAR\_010926.  
 FT CONFLICT 475 475 K -> KO.  
 FT CONFLICT 554 554 E -> Q (IN REF. 3).  
 FT CONFLICT 638 638 M -> I (IN REF. 3).  
 FT CONFLICT 663 663 E -> G (IN REF. 3).  
 FT CONFLICT 913 913 R -> S (IN REF. 3).  
 FT CONFLICT 956 956 N -> S (IN REF. 3).  
 FT CONFLICT 980 982 H -> N (IN REF. 3).  
 FT CONFLICT 997 997 K -> R (IN REF. 1 AND 2).  
 FT CONFLICT 1001 1001 Q -> P (IN REF. 1 AND 2).  
 FT CONFLICT 1020 1020 R -> D (IN REF. 3).  
 FT CONFLICT 1028 1028 V -> E (IN REF. 3).  
 FT CONFLICT 1626 1626 R -> P (IN REF. 1 AND 2).  
 FT CONFLICT 1703 1703 N -> T (IN REF. 3).  
 FT CONFLICT 1707 1707 V -> G (IN REF. 3).  
 FT CONFLICT 1802 1803 MISSING (IN REF. 5).  
 FT CONFLICT 1843 1843 A -> P (IN REF. 3).  
 FT CONFLICT 1956 1956 I -> V (IN REF. 3).  
 FT CONFLICT 2027 2027 V -> D (IN REF. 5).  
 FT CONFLICT 2157 2158 EI -> HE (IN REF. 7).  
 FT CONFLICT 2169 2169 E -> V (IN REF. 3).  
 FT CONFLICT 2514 2514 L -> R (IN REF. 3).  
 FT CONFLICT 2851 2851 I -> N (IN REF. 8).  
 FT CONFLICT 2957 2957 E -> D (IN REF. 3).  
 FT CONFLICT 2983 2983 P -> S (IN REF. 3, 7 AND 8).  
 FT CONFLICT 3087 3087 O -> H (IN REF. 3).  
 FT CONFLICT 3218 3218 Q -> H (IN REF. 3).  
 FT CONFLICT 3307 3309 ESE -> OSQ (IN REF. 3).  
 FT CONFLICT 3751 3751 P -> A (IN REF. 3).  
 FT CONFLICT 3833 3833 T -> S (IN REF. 3).  
 SQ SEQUENCE 3911 AA; 453664 MW; 3FBQCB1C819B4/AA CRC64;

Query Match 6.8%; Score 162.5; DB 1; Length 3911;  
 Best Local Similarity 22.2%; Pred. No. 1.2;  
 Matches 96; Conservative 80; Mismatches 176; Indels 81; Gaps 18;

QY 83 LDNVRQLSQKD---KEKRSQVIIIDLRTL-----BERNA 116  
 Db 1999 AGVEQEOLQETEKLMEKFLEVOCQAFKVRODLOQVKALEIDTVEQSRTFELQEKNT 2058  
 QY 117 TVVSLQQALGKAEMLCSTLUKKOMYKLEQQ---QDETQAOBEAGRURSKMTMEIELL 172  
 Db 2059 ELMDLRQ - -QNOALEKOLEKMRKFLDEQAIDREHERDVFOEQIOKLEQQLKVVPREFQPI 2115  
 QY 173 LGSQLPVELEM RDGMGQGSQSAVELAYCVSUKKE -ENLFARKASGEWADLKREDLES 231  
 Db 2116 SEHOTREVEQANHLKEKTDKCELLSKEQLQRDQTOERNEEIEKLEFRVRB-LEQALLY 2174  
 QY 232 SRSKLQTYVSELD - -OAKLEIK ---SAOKD - -SADKREIMSIKKLTMQETINLP 281  
 Db 2175 SADTFQKVEDRHFGAVEYAKPELVEQYDRAIDRKETTNLEQFQEFREELE - 2232  
 QY 282 PVASETVDRLL-----ESPAPEVNLLRPPSFRRDIDNATFDVTPPARPSSSH 334  
 Db 2223 -NKNEEVQCLHMOLEIQKKESTRILQ ELEQENKLFKDMDM KGLAIKESDAMSTQDH 2289  
 QY 335 GYEKLC --LEKSHSP TQDVPKICKOPPRKESOLSLGGQSCAGERDPELVCAFPIVNA 392  
 Db 2290 VLGCKFAQTIEKEVEIDOLNEQVTK --LQQQLKITTDNKVIEKENELIRDLETQIECL 2346  
 QY 393 ILGOKQPKPRSE 405  
 Db 2347 MSDOECVNRNRE 2359

Search completed: September 4, 2002, 16:17:19  
 Job time: 478 sec

Thu Sep 5 10:01:01 2002

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